

Db 571 EEBGKGGPGPPE 584

RESULT 2

ID 09W485 PRELIMINARY; PRT: 1194 AA.

AC 09W485: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

GN CG3125 protein.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pletlifer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bozskoy S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,

RA Burris K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,

RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McKulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

0960F1

ID 0960F1 PRELIMINARY; PRT: 1284 AA.

AC 0960F1: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN S004165p.

DE S004165p.

GN CG3125.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

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RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

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RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch L., Beasley E.M.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bozskoy S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,

RA Burris K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,

RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA McKulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

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RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

0960F1

ID 0960F1 PRELIMINARY; PRT: 1284 AA.

AC 0960F1: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN S004165p.

DE S004165p.

GN CG3125.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

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RC STRAIN=BERKELEY;

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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

0960F1

ID 0960F1 PRELIMINARY; PRT: 1284 AA.

AC 0960F1: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

GN S004165p.

DE S004165p.

GN CG3125.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

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RA Burris K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,

RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

Query Match 41.2%; Score 51.5; DB 4; Length 681;
Best Local Similarity 54.2%; Pred. No. 20;
Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 1 LDTWVK-----EOKGKGGGAPPK 19
DB 155 LDTWVKFAFSSDEGVGGPAPPK 178

RESULT 5
060307 PRELIMINARY: PRT: 1308 AA.

AC 060307: PRELIMINARY: PRT: 1308 AA.
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE KIAA0561 protein (Fragment).
GN KIAA0561.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 5:31-39(1998).
RN [2]
RP SEQUENCE OF 1-593 FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Gaines J., Liu S.,
Dangnan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
Atlix C., Andeise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
RT PDE4C."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB011133; BAA25487.1;
DR EMBL: AC005793; AAC62830.1;
DR HSSP: P05132; ICTP.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR000961; pkinase_C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00055; PDZ_1.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00228; PDZ_1.
DR SMART: SM00220; S_TKc_1.
DR SMART: SM00133; S_TKc_1.
DR PROSITE: PS50106; PDZ_1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER
SO SEQUENCE 1308 AA; 143004 MW; 983A23C528EF47A6 CRC64;

QY 1 LDTWVK-----EOKGKGGGAPPK 19

DB 782 LDTWVKFAFSSDEGVGGPAPPK 805

RESULT 6
057795 PRELIMINARY: PRT: 153 AA.

AC 057795: PRELIMINARY: PRT: 153 AA.
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein PH0068.
GN PH0068.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OC NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
DR EMBL: AP000001; BAA29137.1;
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 153 AA; 16966 MW; 9063FA186DA9255B CRC64;

Query Match 40.8%; Score 51; DB 17; Length 153;
Best Local Similarity 60.0%; Pred. No. 5;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDTWVKDKGKGGG 15
DB 121 LDTWVKDKGKGGG 135

RESULT 7
095526 PRELIMINARY: PRT: 297 AA.

AC 095526: PRELIMINARY: PRT: 297 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE LD33666P.
GN ANTP OR BG:DS07700.1 OR CG1028.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA Chapple M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nino J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY060407; AAL25446.1;
DR FLYBASE: FBgn0000095; ANTP.
DR InterPro: IPR001827; Antennapedia.
DR PROSITE: PS00032; ANTENNAPEIDIA; UNKNOWN_1.
SO SEQUENCE 297 AA; 32845 MW; A88C5435ABD61983 CRC64;

Query Match 40.8%; Score 51; DB 5; Length 297;

Best Local Similarity 45.0%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MYEOKGKGGAPPKDLMY 23
DB 230 MYOQSGVPVGPAPGGMH 249

RESULT 8

Q8R238 PRELIMINARY; PRT; 224 AA.
AC Q8R238;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01159_D09.31 (TREMBLrel. 21, Last annotation update)
GN 01159_D09.31.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Euphorbiaceae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:01159_D09.31";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AP003792; BAB89213.1, -;
SQ SEQUENCE 224 AA; 22952 MW; 01DB82A5972633F CRC64;

Query Match
Best Local Similarity 40.0%; Score 50; DB 10; Length 224;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEOKGKGGGAP 18
DB 103 KKKKGKGGGLP 115

RESULT 9
Q30097 PRELIMINARY; PRT; 237 AA.
AC Q30097;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN HLA class II HLA-DQ-beta-1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasunaga S.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
EMBL: LA0180; AAA92331.1, -;
DR HSSP: P13760; 2SEB.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00047; 1g_1.
DR Pfam: PF00969; MHC_II_beta; 1.
DR Prodom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IG_C1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Glycoprotein: MHC II; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 237 AA; 27038 MW; 460B53ABCATBC8EA CRC64;

Best Local Similarity 34.8%; Pred. No. 11;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYEOKGKGGAPPKDLMY 23
DB 215 LGLIRORSKRGQPPAGLH 237

RESULT 10

Q30098 PRELIMINARY; PRT; 237 AA.
AC Q30098;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN HLA-DQB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasunaga S.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
EMBL: LA0181; AAA92332.1, -;
DR HSSP: P13760; 2SEB.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00047; 1g_1.
DR Pfam: PF00969; MHC_II_beta; 1.
DR Prodom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IG_C1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Glycoprotein: MHC II; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 237 AA; 27179 MW; 75C1B91440C0D5DF CRC64;

Query Match
Best Local Similarity 40.0%; Score 50; DB 7; Length 237;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYEOKGKGGAPPKDLMY 23
DB 215 LGLIRORSKRGQPPAGLH 237

RESULT 11

Q29970 PRELIMINARY; PRT; 264 AA.
AC Q29970;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN HLA-DW12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88226367; PubMed=3371836;
RA Yasunami M.;
RT "Structural analysis of human major histocompatibility complex class
II genes";
RL Fukunaka Igaku Zasshi 79:153-167(1988).
DR EMBL: M57649; AAA63217.1, -;
DR HSSP: P13760; 2SEB.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000353; MHC_II_beta.

Query Match
40.0%; Score 50; DB 7; Length 237;

DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER
 SQ SEQUENCE 264 AA: 29871 MW: BB6MAA9054F3CB75 CRC64:

Query Match 40.0%; Score 50; DB 7; Length 264;
 Best Local Similarity 34.8%; Pred. No. 13;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 LDTMWKQKGGKGGAPPKDLMY 23
 DB 242 LGIIIRORSQKGGPGGAPGLH 264

RESULT 12

ID Q30155 PRELIMINARY; PRT; 269 AA.
 AC Q30155;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HLA-DRA2 protein.
 GN HLA-DRA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 SEQUENCE FROM N.A.
 RX MEDLINE=87192945; PubMed=3494674;
 RA Tsunamoto K., Yasunami M., Kimura A., Inoko H., Ando A., Hirose T.,
 RA Inayama S., Sasazuki T.;
 RT "DRA1 beta gene from HLA-DRA2-DW12 consists of six exons and expresses
 multiple DRA1 beta polypeptides through alternative splicing.";
 RL Immunogenetics 25:343-346(1987).
 DR EMBL; M16276; AAA59823.1; -.
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 SQ SEQUENCE 269 AA: 30532 MW: 4F81EG5AD92A6EA CRC64:

Query Match 40.0%; Score 50; DB 7; Length 269;
 Best Local Similarity 34.8%; Pred. No. 13;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 LDTMWKQKGGKGGAPPKDLMY 23
 DB 247 LGIIIRORSQKGGPGGAPGLH 269

RESULT 13

ID Q8S1B7 PRELIMINARY; PRT; 497 AA.
 AC Q8S1B7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE B11AB07.4 protein.
 GN B11AB07.4.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Eupharitidae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN (1)
 SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 clone:B11AB07.";
 RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003334; BAB6995.1; -.
 SQ SEQUENCE 497 AA: 55128 MW: B0B9ADBA00DF94C4 CRC64:

Query Match 40.0%; Score 50; DB 10; Length 497;
 Best Local Similarity 61.5%; Pred. No. 24;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KEQKGGKGGAP 18
 DB 378 KKKKGGKGGAP 390

RESULT 14

ID Q9N893 PRELIMINARY; PRT; 611 AA.
 AC Q9N893;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Vir12 protein.
 GN Vir12.
 OS Plasmodium vivax.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5855;
 RN (1)
 SEQUENCE FROM N.A.
 RP Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,
 RA del Portillo H.A., Lanzer M., Barrell B.G.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL360354; CAB96702.1; -.
 SQ SEQUENCE 611 AA: 68442 MW: A642D1893D7D8F4 CRC64:

Query Match 40.0%; Score 50; DB 5; Length 611;
 Best Local Similarity 56.2%; Pred. No. 30;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 MYEQKGGKGGAPPK 19
 DB 366 TKKGGVSPAGSPSK 381

RESULT 15

ID Q74299 PRELIMINARY; PRT; 191 AA.
 AC Q74299;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ORP15 protein precursor.
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenozetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllum; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN (1)
 SEQUENCE FROM N.A.
 RP STRAIN=4-40;
 RA Lugones L.G.;
 RL Thesis (1998), University of Groningen.
 DR EMBL; AJ007503; CAA07544.1; -.
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 191 AA: 19973 MW: 778518F0D830179 CRC64:

Query Match 39.2%; Score 49; DB 3; Length 191;

Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches

4; Indels 0; Gaps 0;

QY 5 VKEQKGKPGGAPPK 19
:::| | | | | | | | | |
Db 90 IEEIKGKRPAGHPPK 104

Search completed: April 11, 2003, 16:14:15
Job time : 8.10277 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 1.35073 Seconds
(without alignments)
706.250 Million cell updates/sec

Title: US-09-821-726a-2

Sequence: 125
1 LDTMYKQKGGKGGAPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	184	1	CLIP_MOUSE
2	90	72.0	199	1	CLIP_MOUSE
3	51	40.8	378	1	HMAN_DROME
4	49	39.2	142	1	PUBB_KLEPNI
5	49	39.2	331	1	TAL_HUMAN
6	47	37.6	233	1	HB2A_RAT
7	47	37.6	263	1	HB2B_RAT
8	46	36.8	267	1	TRUA_CHLMU
9	46	36.8	267	1	TRUA_CHLTR
10	46	36.8	268	1	HB2X_HUMAN
11	46	36.8	398	1	ACOC_BACSU
12	46	36.8	423	1	VJAR_MOUSE
13	46	36.8	697	1	PURL_PYRAE
14	45.5	36.4	402	1	GONI_HUMAN
15	45	36.0	137	1	LSM4_MOUSE
16	45	36.0	139	1	LSM4_MOUSE
17	45	36.0	160	1	PEPD_SCEOB
18	45	36.0	263	1	HB2K_MOUSE
19	45	36.0	263	1	HB2S_MOUSE
20	45	36.0	263	1	HB2U_MOUSE
21	45	36.0	265	1	HB2A_MOUSE
22	45	36.0	265	1	HB2D_MOUSE
23	45	36.0	265	1	HB2O_MOUSE
24	45	36.0	302	1	CCDC_CAEEL
25	45	36.0	863	1	AXNI_MOUSE
26	45	36.0	863	1	POIG_TBREYH
27	45	36.0	3414	1	POIG_TBREYH
28	44.5	35.6	264	1	COLI_MACNE
29	44.5	35.6	267	1	COLI_HUMAN
30	44.5	35.6	267	1	COLI_PIG
31	44.5	35.6	311	1	MRAM_CAUCR
32	44	35.2	172	1	CH18_DROME
33	44	35.2	231	1	DEOC_THETN

34	44	35.2	275	1	CAB4_HUMAN	P57796 homo sapien
35	44	35.2	375	1	SOX3_MOUSE	P53784 mus musculus
36	44	35.2	471	1	SLA_YARLI	P78979 Yarrowia li
37	44	35.2	479	1	PGRC_LEIME	O27686 leishmania
38	44	35.2	506	1	CP4B_RABIT	P15128 oryctolagus
39	44	35.2	540	1	CH61_SYNY3	O05972 synechocyst
40	44	35.2	546	1	RUB1_BRANA	P21239 brassica na
41	44	35.2	550	1	GPE1_CHICK	P50593 gallus gall
42	44	35.2	783	1	CAD5_MOUSE	P55284 mus musculus
43	43.5	34.8	212	1	COLI_SHEEP	P01191 o corticotr
44	43.5	34.8	265	1	COLI_BOVIN	P01190 b corticotr
45	43.5	34.8	431	1	HXB3_HUMAN	P14651 homo sapien

ALIGNMENTS

RESULT 1
CLIP_MOUSE STANDARD; PRT: 184 AA.
ID CLIP_MOUSE
AC O9CR36: O9D7K7: O9CT25:
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CALL protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guncioncin S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
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DR EMBL; AK008990; BAB26010.1;
DR EMBL; AK008622; BAB25784.1;
DR EMBL; AK008641; BAB25801.1;
DR EMBL; AK008647; BAB25805.1;
DR EMBL; AK008722; BAB25856.1;
DR EMBL; AK008745; BAB25872.1;
DR EMBL; AK008933; BAB25975.1;
DR EMBL; AK008956; BAB25988.1;
DR EMBL; AK009145; BAB26103.1;
DR EMBL; AK019050; BAB31525.1;

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DR EMBL; M29097; AAA61979.1; .
DR PIR; D32880; D32880.
FW Hypothetical protein.
FT NON_TER 142
SQ SEQUENCE 142 AA; 16447 MW; 03ED03FBF63242D0 CRC64;

Query Match
Best local Similarity 39.2%; Score 49; DB 1; Length 142;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QKKGKPGCAPK 19
DB 49 RKKGKGGKPPR 60

RESULT 5

TAL_HUMAN
ID TAL_HUMAN STANDARD; PRT; 331 AA.
AC P17342;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell acute lymphocytic leukemia-1 protein (TAL-1 protein) (STEM cell protein) (T-cell leukemia/lymphoma-5 protein).
GN TAL1 OR SCL OR TC15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI-TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA MEDLINE=91061750; PubMed=2247063;
RA Apian P.D., Begley C.G., Bertness V., Nussmeier M., Ezquerria A., Coligan J., Kirsch I.R.;
RT "The SCL gene is formed from a transcriptionally complex locus."
RL Mol. Cell. Biol. 10:6426-6435(1990).
RP SEQUENCE FROM N.A.
RA Grafham D.;
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RC [3]
RP SEQUENCE OF 118-331 FROM N.A.
RC TISSUE=bone marrow;
RA MEDLINE=90099309; PubMed=2602361;
RA Begley C.G., Apian P.D., Denning S.M., Haynes B.F., Waldmann T.A., Kirsch I.R.;
RT "The gene SCL is expressed during early hematopoiesis and encodes a differentiation-related DNA-binding motif."
RL Proc. Natl. Acad. Sci. U.S.A. 86:10128-10132(1989).
RN [4]
RP SEQUENCE OF 181-331 FROM N.A.
RA MEDLINE=90151616; PubMed=2301035;
RA Chen Q., Cheng J.-T., Tsai L.H., Schneider N., Buchanan G., Carroll A., Crist W., Ozanne B., Scigliano M.J., Baer R.;
RT "The tal gene undergoes chromosome translocation in T cell leukemia and potentially encodes a helix-loop-helix protein."
RL EMBO J. 9:415-424(1990).
RP SEQUENCE OF 106-148 FROM N.A.
RA MEDLINE=91037802; PubMed=2230650;
RA Chen Q., Yang C.Y.C., Tsan J.T., Xia Y., Ragab A.H., Peiper S.C., Carroll A., Baer R.;
RT "Coding sequences of the tal-1 gene are disrupted by chromosome translocation in human T cell leukemia."
RL J. Exp. Med. 172:1403-1408(1990).
RP FUNCTION.
RA MEDLINE=93011002; PubMed=1396592;
RA Apian P.D., Nakahara K., Orkin S.H., Kirsch I.R.;
RT "The SCL gene product: a positive regulator of erythroid

RT differentiation."
RL EMBL J. 11:4073-4081(1992).
RN [7]
RP PHOSPHORYLATION.
RA MEDLINE=93173511; PubMed=8437851;
RA Cheng J.-T., Hsu H.-L., Hwang L.-Y., Baer R.;
RT "Products of the TAL1 oncogene: basic helix-loop-helix proteins phosphorylated at serine residues."
RL Oncogene 8:677-683(1993).
CC [1]
CC IT MAY PLAY AN IMPORTANT ROLE IN THE GENESIS OF HEMOPOIETIC MALIGNANCIES.
CC SERVES AS A POSITIVE REGULATOR OF ERYTHROID DIFFERENTIATION.
CC TO THE LIM DOMAIN CONTAINING PROTEIN RHOMBOTIN-2.
CC SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC P39-TAL1 AND P22-TAL1; ARE PRODUCED BY ALTERNATIVE SPLICING. THE
CC SPLICING PATTERN IS CELL-LINEAGE DEPENDENT.
CC [1]
CC TISSUE SPECIFICITY: LEUKEMIC STEM CELL.
CC [1]
CC FOR THE INTERACTION WITH DRG1
CC [1]
CC PTM: PHOSPHORYLATED ON SERINE RESIDUES.
CC [1]
CC OF STEM-CELL LEUKEMIA (T-ALL) (A FORM
CC TRANSLOCATION T(1;14)(p32;q11) WHICH INVOLVES TAL1 AND T-CELL
CC RECEPTOR ALPHA CHAIN (TCRA) GENES.
CC [1]
CC SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC [1]
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DR EMBL; M61108; AAA36600.1; .
DR EMBL; M61103; .; NOT_ANNOTATED_CDS.
DR EMBL; M61104; .; NOT_ANNOTATED_CDS.
DR EMBL; M61105; .; NOT_ANNOTATED_CDS.
DR EMBL; M63572; .; NOT_ANNOTATED_CDS.
DR EMBL; AL135960; CAB72103.1; .
DR EMBL; M63589; AAA36599.1; .
DR EMBL; M63576; AAA36599.1; JOINED.
DR EMBL; M29038; AAA36598.1; .
DR EMBL; X51990; CAA36246.1; .
DR EMBL; X58621; CAA36246.1; .
DR EMBL; X58622; CAA36246.1; .
DR PIR; A34519; A34519.
DR TRANSFAC; T00790; .
DR GENE; HGNC:11556; TAL1.
DR MIM; 187040; .
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH_1.
DR SMART; SM00353; HLH_1.
DR PROSITE; PS00038; HLH_1.
DR PROSITE; PS50888; HLH_2; 1.
KW DNA-binding; Transcription regulation; Differentiation;
KW Phosphorylation; Chromosomal translocation; Alternative splicing;
FT DOMAIN 89 132 PRO-RICH.
FT DNA_BIND 187 199 BASIC DOMAIN.
FT DOMAIN 200 240 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 263 274 POLY-GLY.
FT VARSPIC 1 25 MISSING (IN ISOFORM P39-TAL1).
FT VARSPIC 1 175 MISSING (IN ISOFORM P22-TAL1).
SQ SEQUENCE 331 AA; 34270 MW; 33BBE31589DBB7C7 CRC64;

Query Match
Best local Similarity 39.2%; Score 49; DB 1; Length 331;
Matches 69.2%; Pred. No. 9.2;


```

Query Match          37.6%;   Score 47;   DB 1;   Length 263;
Best local Similarity 36.4%;   Pred. No. 14;
Matches            8;   Conservative      5;   Mismatches      9;   Indels      0;   Gaps
Oy      1   LDITWKEQKCGKPGCAPPKDLM 22
          | : : : | | | | :
Db      241  LGLFIRHKQKGPKGPPAGL 262

RESULT 8
TRUA_CHLMU
ID      TRUA_CHLMU      STANDARD;      PRT;      267 AA.
AC      O9PPT0:
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DEF     tRNA pseudouridine synthase A (EC 4.2.1.70) (pseudouridylate synthase
DE      1) (pseudouridine synthase I) (uracil hydrolyase).
DE      GN
TRUA OR TC0748.

```

OS Chlamydia muridarum.
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MOPN / Ni99;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Quinn M., Nelson W., DeBoy R., Kolony J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 pneumoniae AR39";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
 CC 5-phosphate + H(2)O.
 CC -1- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: AE002343; AAF39555.1;
 DR InterPro: IPR001406; Pseudou_synth_1.
 DR Pfam: PF01416; Pseudou_synth_1.
 DR TIGRfams: TIGR00071; hist_trua; 1.
 KW Lyase; trna processing; Complete proteome.
 FT ACT_SITE 52 BY SIMILARITY.
 SQ SEQUENCE 267 AA; 30413 MW; CEBDB356B8EDB87 CRC64;
 Query Match 36.8%; Score 46; DB 1; Length 267;
 Best Local Similarity 42.9%; Pred. No. 20;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Oy 1 LDTWKEOKGKGGPGAPPKDL 21
 Db 221 LEMLEKRRKGGPSPAPPYGL 241
 RESULT 9
 TRUA.CHLTR STANDARD: PRT; 267 AA.
 AC 084469;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE trna pseudouridine synthase A (EC 4.2.1.70) (Pseudouridylylate synthase
 DE I) (Pseudouridine synthase I) (Uracil hydrolase).
 GN TRUA OR CT463.
 OS Chlamydia trachomatis.
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-D/UM-3/CX;
 RX MEDLINE=99000809; PubMed=9784136;
 RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis";
 RL Science 282:754-759(1998).
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN
 CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAs (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine

CC 5'-phosphate + H(2)O.
 CC -1- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: AE001320; AAC68063.1;
 DR InterPro: IPR001406; Pseudou_synth_1.
 DR Pfam: PF01416; Pseudou_synth_1.
 DR TIGRfams: TIGR00071; hist_trua; 1.
 KW Lyase; trna processing; Complete proteome.
 FT ACT_SITE 53 BY SIMILARITY.
 SQ SEQUENCE 267 AA; 30427 MW; 917EX49E394B3CB3 CRC64;
 Query Match 36.8%; Score 46; DB 1; Length 267;
 Best Local Similarity 42.9%; Pred. No. 20;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 LDTWKEOKGKGGPGAPPKDL 21
 Db 221 LDMLATRRKGGPSPAPPYGL 241
 RESULT 10
 HB2X.HUMAN STANDARD: PRT; 268 AA.
 ID HB2X.HUMAN
 AC P05538;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HLA class II histocompatibility antigen, DX beta chain precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=87250501; PubMed=3036828;
 RA Jonsson A.K., Hyldig-Nielsen J.J., Serenius B., Larhammar D.,
 RA Andersson G., Joergensen F., Peterson P.A., Rask L.;
 RT "Class II genes of the human major histocompatibility complex.
 RT Comparisons of the DQ and DX alpha and beta genes";
 RL J. Biol. Chem. 263:8767-8777(1987).
 GN [2]
 OS SEQUENCE OF 38-125 FROM N.A.
 CC MEDLINE=85216510; PubMed=3858830;
 RA Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auffray C.,
 RA Lillie J.W., Grossberger D., Strominger J.L.;
 RT "Gene organization of DC and DX subregions of the human major
 RT histocompatibility complex";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: M29614; -; NOT ANNOTATED CDS.
 DR EMBL: M29615; -; NOT ANNOTATED CDS.
 DR PIR: D29312; D29312.
 DR HSSP: P13760; 2SER.
 DR Genew: HGNC:4945; HLA-DQB2.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003597; I9_c1.

DR InterPro: IPR000353; MHC_II_beta.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00969; MHC_II_beta; 1.
 DR Pfam: PD000328; MHC_II_beta; 1.
 DR SMART: SM00407; Ig1; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW MHC II; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 32
 FT CHAIN 33 268
 FT DOMAIN 33 126
 FT DOMAIN 127 229
 FT TRANSMEM 230 250
 FT DOMAIN 251 268
 FT DISULFID 47 110
 FT DISULFID 148 204
 FT CARBOHYD 51 51
 SO SEQUENCE 268 AA; 30386 MW; 2746ED6CC5D44AF2 CRC64;

Query Match 36.8%; Score 46; DB 1; Length 268;
 Best Local Similarity 34.8%; Pred. No. 20;
 Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 1 LDTWKEQKCKGPGAPPKDLMY 23
 I : : : : | | | | | : :
 DB 246 LGLIRHRCQKGRGPPAGLH 268

RESULT 11
 ACOC_BACSU STANDARD; PRT; 398 AA.
 ID ACOC_BACSU
 AC 031550;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Dihydroilpoamide acetyltransferase component of acetoin cleaving
 DE system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component).
 GN ACOC.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AC327;
 RX MEDLINE=97124190; PubMed=8969503;
 RA Yamamoto H., Uchiyama S., Sekiguchi J.;
 RT Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76
 RT degrees region of the Bacillus subtilis chromosome containing genes
 RT for trehalose metabolism and acetoin utilization.";
 RL Microbiology 142:3057-3065(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brilgen S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano N.J., Carter R.A.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings S.D., Emmerson P.T.,
 RA Denliot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Foulger D.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleton N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Hatesch J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Ilaya M., Jones L.,
 RA Joris B., Katamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Patro V., Pohl T.M., Portetelle D., Portollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serrif P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassatoli A.,
 RA Viari A., Wambut R., Wedler E., Yamane K., Yasumoto K., Yata K.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yoshikawa H., Danchin A.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RT Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydroilpoamide = CoA + S-
 CC acetyl-dihydroilpoamide
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC -1- COFACTOR (PROBABLE).
 CC -1- PATHWAY: Acetoin catabolism.
 CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
 CC -----
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 CC -----
 CC EMBL: D78509; BAA24294.1; -;
 CC EMBL: Z99108; CAB12637.1; -;
 CC HSSP: P07016; 1BLI.
 CC Subtilist; BG12560; ACOC.
 CC InterPro: IPR001078; 2oxoacid.dh.
 CC InterPro: IPR000089; Biotin.lipoyl.
 CC InterPro: IPR004167; E3 binding.
 CC InterPro: IPR003016; lipoyl.
 CC InterPro: IPR00198; 2-oxoacid.dh; 1.
 CC Pfam: PF00198; 2-oxoacid.dh; 1.
 CC Pfam: PF02817; e3 binding; 1.
 CC Pfam: PF00364; biotin.lipoyl; 1.
 CC ProDom: PD001115; 2oxoacid.dh; 1.
 CC PROSITE: PS00189; LIPOYL; FALSE-NEG.
 CC TRANSFERASE; Acyltransferase; Lipoyl; Complete proteome.
 KW DOMAIN 1 76
 FT BINDING 43 43
 FT ACT_SITE 371 371
 FT ACT_SITE 375 375
 FT ACT_SITE 375 375
 SO SEQUENCE 398 AA; 42885 MW; 559564C27C1C64F6 CRC64;

Query Match 36.8%; Score 46; DB 1; Length 398;
 Best Local Similarity 56.2%; Pred. No. 29;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 5 VKEQKGPFGAPPKD 20
 I : : | | | | | |
 DB 134 LKOLKGTGPGGRIVKD 149

RESULT 12
 VIAR_MOUSE STANDARD; PRT; 423 AA.
 ID VIAR_MOUSE
 AC 062463; 062464; 090YH2;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Vasopressin Via receptor (VIAR) (Vascular/hepatic-type arginine
 DE vasopressin receptor) (Antidiuretic hormone receptor 1a) (AVPR 1la).
 GN AVPR1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match	36.8%	Score 46	DB 1	Length 423
Best Local Similarity	50.0%	Pred No. 31		
Matches 8: Conservative	3	Mismatches	5	Indels
				Gaps 0
QY	6 KEQKRGPGAGPPKL	21		
	: : : : : : : : :			
Db	30 KEAAGLGEGGSPPGDV	45		

RESULT 13	PURL_PYRAE	STANDARD;	PRT;	697 AA.
ID	PURL_PYRAE			
AC	08227;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAM			

Query Match	36.8%	Score 46;	DB 1;	Length 697;
Best Local Similarity	50.0%;	Pred. No. 51;		
Matches	9;	Conservative	3;	Mismatches 6;
				Indels 0;
				Gaps 0;
QY	5	VKQKCKGPGAGAPKDDM	22	
	:			
Db	173	IVKDGVPVPGAGAPGDLI	190	

ID	GONI_HUMIN	STANDARD:	PRT:	402 AA.
AC	P56680;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, last sequence update)			
DT	15-JUL-1999 (Rel. 38, last annotation update)			
DE	Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (cellulase)			
GN	Cel7B.			
OS	Humicola insolens.			
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.			
OX	NCBI_taxid=34413;			
RN	[1]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.			
RX	MEDLINE=97415713; PubMed=9335168;			
RA	Volosaccharide specificity of a family 7 endoglucanase: insertion			
RT	of potential sugar-binding subsites.";			
RL	J. Biotechnol. 57:91-100(1997).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.			
RX	MEDLINE=98437137; PubMed=9761741;			
RA	MacKenzie L.F., Sulzenbacher G., Digne C., Jones T.A., Woeldike H.F.			
RT	Schaeuble M., Withers S.G., Davies G.J.			
	"Crystal structure of the family 7 endoglucanase I (cel7B) from			

```

RT Humicola insolens at 2.2 A resolution and identification of the
RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
RT intermediate."
RL Biochem. J. 335:409-416(1998).
CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
CC (1) EXOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
CC (2) ENDOCELLULOHYDROLASES THAT CUT THE DISSACCHARIDE CELLULOSE
CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN:
CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL
CC HYDROLASES).
DR PDB: 1A39; 02-MAR-99.
DR PDB: 2A39; 16-FEB-99.
DR InterPro: IPR001722; GH_7.
DR Pfam: PF00840; Glyco_hydro_7; 1.
DR ProDom: PD186135; GH_7; 1.
DR Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 197 197 NUCLEOPHILE.
FT ACT_SITE 202 202 PROTON DONOR.
FT DISULFID 18 24
FT DISULFID 51 73
FT DISULFID 63 69
FT DISULFID 140 365
FT DISULFID 172 195
FT DISULFID 176 194
FT DISULFID 215 234
FT DISULFID 223 228
FT DISULFID 239 315
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 36.4%; Score 45.5; DB 1; Length 402;
Best Local Similarity 36.7%; Pred. No. 35;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKQKGGKPGGA-----PPKDL 21
   |||: : : ||||| ||||:
DB 33 LDSLSPHHRREGGLGPGCGDMGNPPKDV 62

RESULT 15
LSM4_MOUSE
ID LSM4_MOUSE STANDARD: PRT; 137 AA.
AC O90XA5:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE U6 snRNA-associated Sm-like protein Lsm4.
GN LSM4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20094984; PubMed=10629062;
RA Hirsch E., Ohashi T., Ahmad M., Stamm S., Faessler R.;
RT "Peri-implantation lethality in mice lacking the sm motif-containing
RT protein Lsm4."
RL Mol. Cell. Biol. 20:1055-1062(2000).
CC -1- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
CC snRNA (BY SIMILARITY).
CC -1- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGNOT SHAPE.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

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CC -1- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
CC -----
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CC -----
DR EMBL: AJ249439; CAB65729.1; -.
DR HSSP: P43331; ID3B.
DR MCD: MGI:1354692; Lsm4.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
DR Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 137 AA; 15076 MW; A917E16E1467940 CRC64;

Query Match 36.0%; Score 45; DB 1; Length 137;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGGKPGGA 16
   ||||: |||
DB 95 KQKGRGKGGA 105

Search completed: April 11, 2003, 16:11:50
Job time : 2.5174 secs

```


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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 2.47635 Seconds
(without alignments)
892.885 Million cell updates/sec

Title: US-09-821-726A-2

Perfect score: 125
Sequence: 1 LDTMKRQKKGKGGGAPKDLMY 23

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59	47.2	1677	2	T14267	Xin protein, stage
2	51	40.8	153	2	B71226	hypothetical prote
3	51	40.8	298	2	A49630	ubiquitin conjugat
4	51	40.8	378	2	A25399	homeotic protein A
5	50	40.0	269	2	I54432	MHC class II histo
6	49	39.2	142	2	B32880	hypothetical prote
7	49	39.2	266	2	B84351	pseudouridylylate sy
8	48	38.4	331	2	T50596	T-cell acute lymph
9	48	37.6	218	2	T51887	probable oxidoredu
10	47	37.6	233	1	HLRTAB	hypothetical prote
11	47	37.6	263	1	HLRTAB	R11 class II histo
12	47	37.6	598	2	T42070	protein serine/thr
13	47	37.6	739	2	T49456	hypothetical prote
14	47	37.6	4936	2	A42515	hypothetical prote
15	46	37.2	1240	2	T30834	nuclear protein SA
16	46	36.8	267	2	D81669	tRNA pseudouridine
17	46	36.8	267	2	C71511	probable pseudouri
18	46	36.8	268	2	D29312	MHC class II histo
19	46	36.8	315	2	T29525	hypothetical prote
20	46	36.8	398	2	F69581	acetoin dehydrogen
21	46	36.8	511	2	S24345	Balbani ring 1 pr
22	46	36.8	709	2	T34706	fatty acid oxidati
23	46	36.8	886	2	S07132	hypothetical prote
24	46	36.8	2022	2	T48818	glucan 1,4-alpha-g
25	46	36.8	4957	2	T03455	ALR protein - huma
26	46	36.8	5262	2	T03454	ALR protein - huma
27	45.5	36.4	376	2	A12339	dihydroxylate oxi
28	45.5	36.4	579	2	D72092	conserved hypothet

30	45.5	36.4	579	2	C86532	CT082 hypothetical
31	45	36.0	160	1	S05340	plastoquinol-plast
32	45	36.0	233	2	I59495	major histocompati
33	45	36.0	238	2	A53278	MHC class II histo
34	45	36.0	263	1	HLMSBK	H-2 class II histo
35	45	36.0	263	1	HLMSBU	MHC class II histo
36	45	36.0	263	1	HLMSBS	H-2 class II histo
37	45	36.0	263	2	A61389	MHC class II histo
38	45	36.0	263	2	A25911	H-2 class II histo
39	45	36.0	265	1	HLMSAB	MHC class II histo
40	45	36.0	265	1	HLMSQB	MHC class II histo
41	45	36.0	265	2	I48656	histocompatibility
42	45	36.0	302	2	A31921	collagen dpy-13 pr
43	45	36.0	394	2	S26492	homeotic protein A
44	45	36.0	472	2	T03169	probable glycoprot
45	45	36.0	596	2	T52331	pectinesterase (EC

ALIGNMENTS

RESULT 1
T14267
Xin protein, stage early embryo - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14267
R:Wang, D.Z.; Lin, J.J.C.
Submitted to the EMBL Data Library, March 1998
A:Description: Involvement of a novel gene, Xin, in cardiac looping.
A:Reference number: Z17948
A:Accession: T14267
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1677 <MAN>
A:Cross-references: EMBL:AF051945; NID:q2970645; PID:q2970646; PIDN:AAC06023.1
A:Experimental source: cardiac muscle; stage early embryo

Query Match
Best Local Similarity 47.2%; Score 59; DB 2; Length 1677;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 KEOKGKGGAPK 19
DB 571 EBERKGGPPPE 584

RESULT 2
B71226
hypothetical protein PH0068 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: B71226
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushiida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: B71226
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-153 <KAN>
A:Cross-references: GB:AP000001; NID:q3236128; PIDN:BAA29137.1; PID:q3256454
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genba
C:Genetics:
A:Gene: PH0068
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0068

Query Match
Best Local Similarity 40.8%; Score 51; DB 2; Length 153;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDTWKEQKGGPGG 15
 Db 121 LDTWKEQKGGPGG 135

RESULT 3

ubiquitin conjugating enzyme - human (fragment)
 A:Accession: A49630
 C:Species: Homo sapiens (man)
 C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
 C:Accession: A49630
 R:Plon, S.E.; Lepply, K.A.; Do, H.N.; Groudine, M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10484-10488, 1993
 A:Title: Cloning of the human homolog of the CDC34 cell cycle gene by complementation in
 A:Reference number: A49630; MUID:94068425; PMID:8248134
 A:Accession: A49630
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Cross-references: GB:L22005; NID:g388308; PIDN:AA037534.1; PID:g388309
 C:Superfamily: human ubiquitin-protein ligase E2

Query Match 40.8%; Score 51; DB 2; Length 298;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 KEQKGGPGGAPP 18
 Db 21 EEFGGPGGSGSP 33

RESULT 4

homeotic protein Antennapedia - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jun-2000
 C:Accession: A23450; A23450; A23450; A03318; C24780; S02593
 R:Shenawaty, S.; Kuroiwa, A.; Baumgartner, P.; Gehring, W.J.
 EMBO J. 5, 733-739, 1986
 A:Title: Structural organization and sequence of the homeotic gene Antennapedia of Drosophila
 A:Reference number: A23450; MUID:9334708; PMID:10408949
 A:Accession: A23450
 A:Molecule type: DNA; mRNA
 A:Residues: 1-378 <SCB>
 R:Laughon, A.; Boulet, A.M.; Bermingham Jr., J.R.; Laymon, R.A.; Scott, M.P.
 Mol. Cell. Biol. 6, 4676-4689, 1986
 A:Title: Structure of transcripts from the homeotic antennapedia gene of Drosophila melanogaster
 A:Reference number: A25400; MUID:87089829; PMID:2879223
 A:Accession: A25400
 A:Molecule type: DNA
 A:Residues: 1-378 <LAU>
 A:Cross-references: GB:M4496; GB:K01950; NID:g156945; PIDN:AA028376.1; PID:g156947
 R:Strother, V.L.; Jorgensen, E.M.; Garber, R.L.
 Mol. Cell. Biol. 6, 4667-4675, 1986
 A:Title: Multiple transcripts from the antennapedia gene of Drosophila melanogaster.
 A:Accession: A25399; MUID:87089828; PMID:2879222
 A:Accession: A25399
 A:Molecule type: mRNA
 A:Residues: 1-378 <STR>
 A:Cross-references: GB:M20704; GB:M14699; GB:M14701; NID:g156948; PIDN:AA020214.1; PID:g156949
 R:McGinnis, W.; Garber, R.L.; Wirtz, J.; Kuroiwa, A.; Gehring, W.J.
 Cell 37, 403-408, 1984
 A:Title: A homologous protein-coding sequence in Drosophila homeotic genes and its conse
 A:Reference number: A90847; MUID:84205674; PMID:6327065
 A:Accession: A03318
 A:Molecule type: DNA
 A:Residues: 296-362, 'D' <MCG>
 A:Cross-references: GB:K01948; NID:g156931; PIDN:AA028373.1; PID:g156934
 R:Regulski, M.; Harding, K.; Kostriken, R.; Karch, F.; Levine, M.; McGinnis, W.
 Cell 43, 71-80, 1985
 A:Title: Homeo box genes of the Antennapedia and Bithorax complexes of Drosophila.

A:Reference number: A90874; MUID:86079516; PMID:2416463
 A:Accession: C24780
 A:Molecule type: DNA
 A:Residues: 297-299, 'E', 301-357 <REG>
 A:Cross-references: GB:M12009; NID:g156939; PIDN:AA072241.1; PID:g156940
 A:Note: the authors translated the codon GAA for residue 300 as Gly and TAC for resid
 R:Bermingham Jr., J.R.; Scott, M.P.
 EMBO J. 7, 3211-3222, 1988
 A:Title: Developmentally regulated alternative splicing of transcripts from the Drosophila
 A:Reference number: S02593; MUID:89030617; PMID:2903048
 A:Contents: annotation; alternative splicing
 C:Comment: This homeotic protein controls development of cells in the mesothorax segm
 C:Genetics:
 A:Gene: FlyBase:Antp
 A:Cross-references: FlyBase:Fgn0000095
 A:Map position: 3A47.8; 84B1-2
 A:Introns: 207/3; 220/3; 296/1
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regul
 F:298-354/Domain: homeobox homology <HOX>

Query Match 40.8%; Score 51; DB 2; Length 378;
 Best Local Similarity 45.0%; Pred. No. 15;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 4 MYEQKGGPGGAPPKDLWY 23
 Db 230 MYEQKGGPGGAPPKDLWY 249

RESULT 5

MHC class II histocompatibility antigen DQ α -beta chain precursor - human
 N:Alternate names: cell surface glycoprotein DQ α ; HLA-DQ α
 C:Species: Homo sapiens (man)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 05-May-2000
 C:Accession: I54432; I67725; I68723; I59623
 R:Tsukamoto, K.; Yasunami, M.; Kimura, A.; Inoko, H.; Ando, A.; Hirose, T.; Inayama, Y.
 Immunogenetics 25, 343-346, 1987
 A:Title: DQ α beta gene from HLA-DR2-DW12 consists of six exons and expresses multiple
 A:Reference number: I54432; MUID:87192945; PMID:3494674
 A:Accession: I54432
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <TSU>
 A:Cross-references: GB:M16276; NID:g188397; PIDN:AA059823.1; PID:g307272
 R:Yasunami, M.
 Fukuoka Igaku Zasshi 79, 153-167, 1988
 A:Title: Structural analysis of human major histocompatibility complex class II gene
 A:Reference number: I53630; MUID:88226367; PMID:3371836
 A:Accession: I67725
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 6-269 <FKU>
 A:Cross-references: GB:M57649; NID:g187852; PIDN:AA063217.1; PID:g187853
 R:Lee, B.S.; Bell, J.I.; Rust, N.A.; McDevitt, H.O.
 Immunogenetics 26, 85-91, 1987
 A:Title: Structural and functional variability among DQ beta alleles of DR2 subtypes.
 A:Reference number: I54440; MUID:87278366; PMID:2886427
 A:Accession: I68723
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 33-83, 'P', 85-122 <LEE>
 A:Cross-references: GB:M17204; NID:g187906; PIDN:AA059698.1; PID:g187907
 R:Singal, D.P.; Qiu, X.; Sood, S.K.
 Tissue Antigens 40, 104-107, 1992
 A:Title: Molecular analysis of novel HLA-DR2-DQ α haplotypes in Asian Indians.
 A:Reference number: I59623; MUID:93031783; PMID:1412415
 A:Accession: I59623
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 45-83, 'P', 85-112 <SIN>
 A:Cross-references: GB:M86740; NID:g188221; PIDN:AA059778.1; PID:g188222

OY 10 GKGGGAPPKD 20
 |||||: 1
 Db 433 GKGGGAPPAD 443

RESULT 14

T49456
 hypothetical protein alr7304 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49456
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, May 2000
 A:Reference number: Z25022
 A:Accession: T49456
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-739 <SCH>
 A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:BI4D6.80
 A:Experimental source: BAC clone BI4D6; strain OR74A
 C:Genetics:
 A:Gene: NCSP:BI4D6.80
 A:Map position: 6

Query Match 37.6%; Score 47; DB 2; Length 739;
 Best Local Similarity 61.5%; Pred. No. 1e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 6 KEOKGKGGAPPK 18
 :|||||
 Db 217 REOKGKGPASTP 229

RESULT 15

AH2515
 hypothetical protein alr7304 [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120a1
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AH2515
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AH2515
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-4936 <KUR>
 A:Cross-references: GB:BA000020; PIDN:BA878388.1; PID:917135842; GSPDB:GN00180
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr7304
 A:Genome: plasmid

Query Match 37.6%; Score 47; DB 2; Length 4936;
 Best Local Similarity 40.0%; Pred. No. 6.9e+02;
 Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 OY 1 LDTVMKEQKGGGAPPKD 20
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 Db 2312 VDDGIEONGRPNPDPKD 2331

Search completed: April 11, 2003, 16:15:26
 Job time : 4.47635 secs

Mon Apr 14 14:02:26 2003

us-09-821-726a-2.rapb

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 : Search time 2.28874 Seconds
(without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726a-2

Perfect score: 125
Sequence: 1 LDTWKEQKGGKPGGAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications-AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	72.0	182	US-10-050-704-212	Sequence 212, App
2	90	72.0	185	US-09-992-598-211	Sequence 211, App
3	90	72.0	185	US-09-989-293A-211	Sequence 211, App
4	90	72.0	185	US-09-989-735-211	Sequence 211, App
5	90	72.0	185	US-09-990-444-211	Sequence 211, App
6	90	72.0	185	US-10-001-054-14	Sequence 14, App
7	90	72.0	185	US-09-989-730-211	Sequence 211, App
8	90	72.0	185	US-09-990-436-211	Sequence 211, App
9	90	72.0	185	US-09-991-181-211	Sequence 211, App
10	90	72.0	185	US-09-993-687-211	Sequence 211, App
11	90	72.0	185	US-09-989-734-211	Sequence 211, App
12	90	72.0	185	US-09-997-653-211	Sequence 211, App
13	90	72.0	185	US-09-993-667-211	Sequence 211, App
14	90	72.0	185	US-09-990-438-211	Sequence 211, App
15	90	72.0	185	US-09-990-562-211	Sequence 211, App
16	90	72.0	185	US-09-997-428-211	Sequence 211, App
17	90	72.0	185	US-09-997-666-211	Sequence 211, App
18	90	72.0	185	US-10-227-884-148	Sequence 148, App
19	90	72.0	185	US-09-990-711-211	Sequence 211, App

20	90	72.0	185	US-10-230-163-148	Sequence 148, App
21	90	72.0	185	US-09-989-726-211	Sequence 211, App
22	90	72.0	185	US-09-746-783-146	Sequence 146, App
23	90	72.0	185	US-09-990-437-211	Sequence 211, App
24	90	72.0	185	US-09-998-156-211	Sequence 211, App
25	90	72.0	185	US-10-218-631-148	Sequence 148, App
26	90	72.0	185	US-10-230-338-148	Sequence 148, App
27	90	72.0	185	US-09-991-157-211	Sequence 211, App
28	90	72.0	185	US-09-991-172-211	Sequence 211, App
29	90	72.0	185	US-09-997-514-211	Sequence 211, App
30	90	72.0	185	US-09-997-573-211	Sequence 105, App
31	90	72.0	185	US-10-050-704-105	Sequence 105, App
32	90	72.0	185	US-10-230-414-148	Sequence 211, App
33	90	72.0	185	US-09-990-443-211	Sequence 211, App
34	90	72.0	185	US-09-990-726-211	Sequence 211, App
35	90	72.0	185	US-09-997-559-211	Sequence 211, App
36	90	72.0	185	US-09-997-601-211	Sequence 211, App
37	90	72.0	185	US-09-989-729A-211	Sequence 211, App
38	90	72.0	185	US-09-991-854-211	Sequence 211, App
39	90	72.0	185	US-09-997-349-211	Sequence 211, App
40	90	72.0	185	US-09-997-440-211	Sequence 211, App
41	90	72.0	185	US-09-997-628-211	Sequence 211, App
42	90	72.0	185	US-09-997-683-211	Sequence 211, App
43	90	72.0	185	US-09-989-722-211	Sequence 211, App
44	90	72.0	185	US-09-989-723-211	Sequence 211, App
45	90	72.0	185	US-09-989-723-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-10-050-704-212
Sequence 212, Application US/10050704
Publication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P203991
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/684,524
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: PCT/US00/08979
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,693
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 60/130,991
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 212
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-704-212
Query Match 72.0%; Score 90; DB 9; Length 182;
Best Local Similarity 72.0%; Pred. No. 3.5e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
Oy 1 LDTWKEQK--GKGGGAPPKDLMY 23
||:||||:||||| ||| ||| |||
Db 97 LDTWKEQKKGKGGGAPPKDLMY 121
RESULT 2
US-09-992-598-211
Sequence 211, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertlisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C20
 CURRENT APPLICATION NUMBER: US/09/992,598
 PRIOR FILING DATE: 1997-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
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 PRIOR APPLICATION NUMBER: 60/090435

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gunney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paonli, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PIC66
 CURRENT APPLICATION NUMBER: US/09/989, 293A
 CURRENT FILING DATE: 2001-11-20
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 PRIOR FILING DATE: 1998-07-09

Query Match 72.0%; Score 90; DB 9; Length 185;
 Best Local Similarity 72.0%; Pred. No. 3, 6e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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 Db 97 LDTMVEOKKIOGKPGGAPPKDLMY 121

RESULT 4
 US-09-989-735-211
 Sequence 211, Application US/09989735
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gottlieb, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C61
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 1997-06-16
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Query Match 72.0%; Score 90; DB 9; Length 185;
 Best Local Similarity 72.0%; Pred. No. 3, 6e-05;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVEOK--GKPGGAPKDLMY 23
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RESULT 5

US-09-990-444-211
 Sequence 211, Application US/09990444
 Publication No. US20020193300A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gunney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Nepler, Mary A.
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 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PIC19
 CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 72.0%; Score 90; DB 9; Length 185;
Best Local Similarity 72.0%; Pred. No. 3; 6e-05;
Matches 18; Conservative 3; Indels 2; Gaps 1;
QY 1 LPTMVEKQK-GKPGGAPPKDLMY 23
DB 97 LPAIVKERRKLGCGGPPPKGLMY 121

RESULT 6
US-10-001-054-14
Sequence 14, Application US/10001054
Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034RIPT
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-30
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PRIOR FILING DATE: 1998-04-24
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PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2001-06-01
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PRIOR FILING DATE: 2001-06-20
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 14
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-001-054-14

Query Match 72.0%; Score 90; DB 9; Length 185;
Best Local Similarity 72.0%; Pred. No. 3,6e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTWKEQK--GKFGCAPPKDLWY 23
DB 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 7
US-09-989-730-211
Sequence 211, Application US/09989730
Publication No. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumanabe, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match
 Best Local Similarity 72.0%; Score 90; DB 9; Length 185;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDJWKEOK--GKGGGAPPKDMY 23
 Db 97 LDALYKRLGKGPPKGLMY 121

RESULT 8
 US-09-990-436-211
 Sequence 211, Application US/09990436
 Publication No. US20020198148A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertlisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavio, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730D1C14
 CURRENT APPLICATION NUMBER: US/09/990,436
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-09

Query Match
Best Local Similarity 72.0%; Score 90; DB 9; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTWKEOK-GKGGGAPPKDLMY 23
DB 97 LDTWKEOKGKGGGAPPKDLMY 121

RESULT 9

US-09-991-181-211
Sequence 211, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Kijavlin, Ivar J.
APPLICANT: Knapier, Mary A.
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APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
PRIOR FILING DATE: 2001-11-16
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GENERAL INFORMATION:									
APPLICANT: Askenazi, Avi J.									
APPLICANT: Baker, Kevin P.									
APPLICANT: Bostein, David									
APPLICANT: Desnoyers, Luc									
APPLICANT: Eaton, Dan L.									
APPLICANT: Ferrara, Napoleone									
APPLICANT: Fong, Sherman									
APPLICANT: Gerber, Hauspeter									
APPLICANT: Gerritsen, Mary E.									
APPLICANT: Goddard, Audrey									
APPLICANT: Godowski, Paul J.									
APPLICANT: Grimaldi, J. Christopher									
APPLICANT: Gunney, Austin L.									
APPLICANT: Kljavin, Ivar J.									
APPLICANT: Napier, Mary A.									
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APPLICANT: Paoni, Nicholas F.									
APPLICANT: Roy, Margaret Ann									
APPLICANT: Stewart, Timothy A.									
APPLICANT: Tumas, Daniel									
APPLICANT: Watanabe, Colin K.									
APPLICANT: Williams, P. Mickey									
APPLICANT: Wood, William I.									
APPLICANT: Zhang, Zemin									
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic									
TITLE OF INVENTION: Acids Encoding the Same									
FILE REFERENCE: P2730P1C11									
CURRENT FILING DATE: 2002-11-14									
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;; PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 72.0%; Score 90; DB 9; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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Mon Apr 14 14:02:26 2003

us-09-821-726a-2.rapb

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RESULT 11
US-09-989-734-211
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Publication No. US2003000531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivat J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC64
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Query Match 72.08; Score 90; DB 9; Length 185;
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; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Falton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 72.08; Score 90; DB 9; Length 185;
Best Local Similarity 72.08; Pred. NO. 3.6e-05; 3; Indels 2; Gaps 1;
Matches 18; Conservative

QY 1 LDTWKEOK--GKPGCAPPKDLWY 23
DB 97 LDALVKEKLLGCKGPGCPPEPKGLWY 121

RESULT 13
US-09-993-667-211
Sequence 211, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Holstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gettisen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730D1C4
 CURRENT APPLICATION NUMBER: US/09/993,667
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 72.0% Score 90: DB 9; Length 185;
 Best Local Similarity 72.0% Pred. No. 3.6e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVEQR--GKPGCAPPKDIMY 23
 DB 97 LDALVKEKRLQKGGPGPPKGLMY 121

RESULT 15
 US-09-990-562-211
 Sequence 211, Application US/09990562
 Publication No. US20030027985A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnovers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C18
 CURRENT APPLICATION NUMBER: 2001-11-14
 PRIOR FILING DATE: 1997-06-16
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Query Match 72.0%; Score 90; DB 9; Length 185;
 Best Local Similarity 72.0%; Pred. No. 3.6e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMVKKEOK--GKGGGAPPKDLMY 23
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 Db 97 LDALVKEKIKLOGKGGGPPPKGLMY 121

Search completed: April 11, 2003, 16:17:41
 Job time : 4.28874 secs

Mon Apr 14 14:02:22 2003

us-09-821-726a-2.rai

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 2.32626 Seconds
(Without alignments)
290.907 Million cell updates/sec

Title: US-09-821-726A-2
Perfect score: 125
Sequence: 1 LDTMYKEDKKGKPGCAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	40.8	298	3	US-08-767-942A-25
2	51	40.8	298	4	US-09-177-165A-23
3	46	36.8	467	4	US-09-002-361-3
4	46	36.8	466	4	US-09-002-361-2
5	45.5	36.4	402	3	US-08-709-974A-1
6	45.5	36.4	402	3	US-08-709-974A-5
7	45.5	36.4	415	2	US-08-833-642A-5
8	45.5	36.4	415	3	US-08-709-974A-4
9	45.5	36.4	415	4	US-09-069-632-1
10	45.5	36.4	435	1	US-08-361-920-27
11	45.5	36.4	435	1	US-08-479-939-27
12	45.5	36.4	435	1	US-08-483-432-27
13	45.5	36.4	435	1	US-09-069-632-3
14	45.5	36.4	435	1	US-08-484-905-119
15	45.5	36.4	435	1	US-08-481-985B-119
16	45.5	36.4	435	1	US-08-370-476-119
17	45.5	36.4	435	1	US-08-207-481-39
18	45.5	36.4	435	1	PCT-US95-02689-41
19	45.5	36.4	435	1	US-08-890-865A-1
20	44.5	35.6	72	4	US-09-217-228-13
21	44.5	35.6	89	4	US-09-217-228-8
22	44.5	35.6	91	4	US-09-217-228-2
23	44.5	35.6	114	4	US-09-217-228-5
24	44.5	35.6	331	4	US-09-217-228-6
25	44.5	35.6	422	4	US-09-217-228-7
26	44.5	35.6	402	2	US-08-709-979A-3
27	44.5	35.6	9	2	US-08-460-890A-57

28	43	34.4	9	3	US-08-167-641C-57	Sequence 57, Appl
29	43	34.4	9	4	US-08-460-971A-57	Sequence 57, Appl
30	43	34.4	9	4	US-08-462-040-57	Sequence 26, Appl
31	43	34.4	321	1	US-08-362-670B-26	Sequence 26, Appl
32	43	34.4	321	3	US-08-333-576C-26	Sequence 26, Appl
33	43	34.4	321	4	US-08-808-324-26	Sequence 26, Appl
34	43	34.4	321	5	PCT-US94-14030A-26	Sequence 11, Appl
35	43	34.4	456	3	US-08-709-974A-11	Sequence 6, Appl
36	43	34.4	456	3	US-08-378-255-6	Sequence 4, Appl
37	43	34.4	880	4	US-09-141-212-2	Sequence 4, Appl
38	43	34.4	880	4	US-09-141-212-4	Sequence 4, Appl
39	43	34.4	880	4	US-09-552-351-4	Sequence 6, Appl
40	43	34.4	880	4	US-09-251-372-6	Sequence 2, Appl
41	43	34.4	880	4	US-09-561-138-2	Sequence 4, Appl
42	43	34.4	880	4	US-09-561-138-6	Sequence 6, Appl
43	43	34.4	880	4	US-09-715-336-6	Sequence 6, Appl
44	43	34.4	880	4	US-09-811-241-6	Sequence 6, Appl
45	43	34.4	880	4	US-09-811-241-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-767-942A-25
Sequence 25, Application US/08767942A
Patent No. 6068982

GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UNDOUBTIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029, 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-1000

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-942A-25

Query Match 40.8% Score 51: DB 3; Length 298;
Best Local Similarity 61.5% Pred. No. 5.5;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KEDKGGGCGAP 18
DB 21 EEDAGGCGGSP 33

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RESULT 2
US-09-177-165A-23
; Sequence 23, Application US/09177165A
; Patent No. 6426205
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; FILE REFERENCE: 11/57,100SUI
; CURRENT FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US/09/177,165A
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/092,443
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-23

Query Match
Best Local Similarity 40.8%; Score 51; DB 4; Length 298;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KRQKKGKGGAGP 18
DB 21 EERAGGGGGSP 33

RESULT 3
US-09-002-361-3
; Sequence 3, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-002-361-3

Query Match
Best Local Similarity 36.8%; Score 46; DB 4; Length 467;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTWKEQKGGPGAGPPKD 20
DB 380 LENTINGARGPAPPPAD 399

RESULT 4
US-09-002-361-2
; Sequence 2, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-002-361-2

Query Match
Best Local Similarity 36.8%; Score 46; DB 4; Length 496;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTWKEQKGGPGAGPPKD 20
DB 409 LENTINGARGPAPPPAD 428

RESULT 5
US-08-709-974A-1
; Sequence 1, Application US/08709974A
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ZIP: 1 READABLE FORM:
COMPUTER TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.41A-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NOS: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1
36.4%: Score 45.5; DB 3; Length 402;
Query Match
Best Local Similarity 36.7%: Pred. No. 48;
5; Mismatches
Matches 11; Conservative
1 IDTMM--VKFOGKRGGA-----PPKDL 21
||||: : : ||||| |||||
33 LDLSLHPHRAEGIDPGGCGDMGNPPKRV 62

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RESULT 6
US-08-709-974A-5
Sequence 5, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch Lein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Grego, Valetta
REGISTRATION NUMBER: 35, 127Y
REFERENCE/DOCCKET NUMBER: 4160, 414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

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US-08-709-974A-5	Score 45.5:	DB 3:	Length 402:	Gaps 2:
Query Match	36.4%:			
Best local Similarity	36.7%:			
Matches 11:	Conservative	5:	Indels	9:
Matches 11:	Conservative	5:	Indels	9:
1 LPTM--VKQKGRGPGA-----PPKDL 21				
: :				
33 LDLSLSPHPIHRAEGDLPGGCGDGMGNPPPKTV 62				
DB				

```

RESULT 7
US-08-833-642A-5
Sequence 5, Application US/08833642A
Patent No. 5883066
GENERAL INFORMATION:
APPLICANT: Ivan M. A. J. Herbots et al.
TITLE OF INVENTION: Liquid Detergent Compositions
Containing Cellulase and Amine
TITLE OF SEQUENCES: 5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackie Ann Zurcher
ADDRESSEE: Dinamore & Shohl LLP
STREET: 255 E. Fifth Street
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833, 642A
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A.
REGISTRATION NUMBER: P42,251
REFERENCE/DOCKET NUMBER: CM551C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8177
TELEFAX: (513) 977-8141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-642A-5
Query Match 36.4% Score 45.5; DB 2; Length 415
Best Local Similarity 36.7%; Pred. No. 49;

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Page 4

Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;
QY 1 LDTM---VKROKRGPGGA-----PPKDL 21
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 8

US-08-709-974A-4
Sequence 4, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch lein, Martin
APPLICANT: Rosholt, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6117664 No. 6117664disk of No. 6117664th America, Inc.
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4160,414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-4

Query Match

Best Local Similarity 36.4%; Score 45.5; DB 3; Length 415;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKROKRGPGGA-----PPKDL 21
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 9

US-09-069-632-1
Sequence 1, Application US/09069632
Patent No. 6261828
GENERAL INFORMATION:
APPLICANT: Lund, Henrik
TITLE OF INVENTION: A Process For Combined Desizing
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6261828 No. 6261828disk of No. 6261828th America, Inc.
CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,632
FILING DATE: 29-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK96/00469
FILING DATE: 15-NOV-1996
APPLICATION NUMBER: 1278/95
FILING DATE: 15-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4588,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-069-632-1

Query Match

Best Local Similarity 36.4%; Score 45.5; DB 4; Length 415;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKROKRGPGGA-----PPKDL 21
Db 33 LDSLSPHRAEGLGPGCGGMGNPPKDV 62

RESULT 10

US-08-361-920-27
Sequence 27, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
APPLICANT: Woelcke, Heile F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5457046 No. 5457046disk of No. 5457046th America, Inc.
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992

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APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA: PCT/DK91/00124
APPLICATION NUMBER: 3435.204-US
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-920-27
Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 52;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;
OY 1 LDTM---VKFGKGGPGGA-----PPKDL 21
11: : : 11111 1111:
53 LDLSHPHRAEGLPGCGCDMGNPPKDV 82
DB

RESULT 11
US-08-479-939-27
Sequence 27, Application US/08479939
Patent No. 5686593
GENERAL INFORMATION:
APPLICANT: Moeldike, Helge F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5686593 No. 5686593disk of No. 5686593th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/479,939
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/361,920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
DB

TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-939-27
Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 52;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;
OY 1 LDTM---VKFGKGGPGGA-----PPKDL 21
11: : : 11111 1111:
53 LDLSHPHRAEGLPGCGCDMGNPPKDV 82
DB

RESULT 12
US-08-483-432-27
Sequence 27, Application US/08483432
Patent No. 5763254
GENERAL INFORMATION:
APPLICANT: Moeldike, Helge F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5763254 No. 5763254disk of No. 5763254th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/483,432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-432-27
Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 52;

Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKRQKGGPGA-----PPKDL 21
11: : : : :
Db 53 LDTLSPIHRAEGIGPGCGDMGNPPKDV 82

RESULT 13

US-09-069-632-3
Sequence 3, Application US/09069632
Patent No. 6261828
GENERAL INFORMATION:
APPLICANT: Lund, Henrik
TITLE OF INVENTION: A Process For Combined Desizing
NUMBER OF SEQUENCES: And Stone-Washing of Dyed Denim
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,632
FILING DATE: 29-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK96/00469
FILING DATE: 15-NOV-1996
APPLICATION NUMBER: 1278/95
FILING DATE: 15-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4588, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-069-632-3

Query Match

Best Local Similarity 36.4%; Score 45.5; DB 4; Length 435;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKRQKGGPGA-----PPKDL 21
11: : : : :
Db 53 LDTLSPIHRAEGIGPGCGDMGNPPKDV 82

RESULT 14

US-08-484-905-119
Sequence 119, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Moltez, Estelle
APPLICANT: Abastado, Jean-Pierre
TITLE OF INVENTION: An Altered Major Histocompatibility
Complex(MHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner

STREET: 1300 I Street, N.W., Suite 700
CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,905

FILING DATE: 07-JUNE-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 03495, 0106-03000

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 119:

SEQUENCE CHARACTERISTICS:

LENGTH: 265 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-484-905-119

Query Match

Best Local Similarity 36.0%; Score 45; DB 2; Length 265;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LDTWKQKGGKGGAPGAPKDL 22
11: : : : :
Db 243 LGLFIRHSOKGPGPPAGLL 264

RESULT 15

US-08-481-985B-119
Sequence 119, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Moltez, Estelle
APPLICANT: Abastado, Jean-Pierre
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,985B
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/801,818
 FILING DATE: 05-DEC-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/792,473
 FILING DATE: 15-NOV-1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03495.0106-04000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 119:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-481-985B-119

Query Match 36.0%; Score 45; DB 3; Length 265;
 Best Local Similarity 36.4%; Pred. No. 36;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 LDTVKEQKGGPGGAPKDDLM 22
 Db 243 LGLFIRHRSGKGGPGPPAGLL 264

Search completed: April 11, 2003, 16:16:33
 Job time: 3.32626 secs

Mon Apr 14 14:02:38 2003

us-09-821-726a-3.ra1

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 : Search time 1.41599 seconds
(without alignments)
290.907 Million cell updates/sec

Title: US-09-821-726a-3
Perfect score: 81
Sequence: 1 KXLOGKGGCGPPK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents-AA:
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	61.7	673	4	US-09-078-347A-2
2	49	60.5	855	4	US-09-813-819-2
3	49	60.5	855	4	US-09-920-048-2
4	45	55.6	402	2	US-08-709-979A-3
5	45	55.6	402	3	US-08-709-974A-1
6	45	55.6	415	2	US-08-833-642A-5
7	45	55.6	415	3	US-08-709-974A-4
8	45	55.6	415	4	US-09-069-632-1
9	45	55.6	415	4	US-08-361-920-27
10	45	55.6	435	1	US-08-479-939-27
11	45	55.6	435	1	US-08-483-632-3
12	45	55.6	435	1	US-09-069-632-3
13	45	55.6	435	1	US-09-817-180-2
14	45	55.6	435	1	US-09-817-180-2
15	45	55.6	435	1	US-09-817-180-2
16	45	55.6	435	1	US-09-817-180-2
17	45	55.6	435	1	US-09-817-180-2
18	45	55.6	435	1	US-09-817-180-2
19	45	55.6	435	1	US-09-817-180-2
20	45	55.6	435	1	US-09-817-180-2
21	45	55.6	435	1	US-09-817-180-2
22	45	55.6	435	1	US-09-817-180-2
23	45	55.6	435	1	US-09-817-180-2
24	45	55.6	435	1	US-09-817-180-2
25	45	55.6	435	1	US-09-817-180-2
26	45	55.6	435	1	US-09-817-180-2
27	45	55.6	435	1	US-09-817-180-2

28	43	53.1	298	5	PCT-US95-02689-41	Sequence 41, Appl
29	43	53.1	311	2	US-08-318-837-9	Sequence 9, Appl1
30	42	51.9	118	1	US-08-393-985-14	Sequence 14, Appl1
31	42	51.9	298	3	US-08-767-942A-25	Sequence 25, Appl1
32	42	51.9	298	4	US-09-177-165A-23	Sequence 23, Appl1
33	42	51.9	494	4	US-09-126-420A-26	Sequence 26, Appl1
34	41.5	51.2	1461	4	US-09-585-887-9	Sequence 9, Appl1
35	41.5	51.2	1461	4	US-09-585-887-9	Sequence 9, Appl1
36	41	50.6	107	3	US-08-478-097A-19	Sequence 19, Appl1
37	41	50.6	124	4	US-08-455-559-11	Sequence 11, Appl1
38	41	50.6	124	4	US-09-145-060-11	Sequence 11, Appl1
39	41	50.6	147	5	PCT-US94-00657-11	Sequence 11, Appl1
40	41	50.6	147	4	US-09-347-833-10	Sequence 10, Appl1
41	41	50.6	437	2	US-08-935-450-8	Sequence 8, Appl1
42	41	50.6	629	3	US-08-464-258B-6	Sequence 6, Appl1
43	41	50.6	3025	6	5223423-3	Sequence 3, Appl1
44	40	49.4	112	2	US-08-301-915-3	Sequence 3, Appl1
45	40	49.4	112	3	US-08-524-694A-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-078-347A-2
Sequence 2, Application US/09078347A
Patent No. 6132968
GENERAL INFORMATION:
APPLICANT: Le, Xiao-Chun
APPLICANT: Weinfield, Michael
TITLE OF INVENTION: Methods for Quantitating Low Level
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,347A
FILING DATE: 13-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UALB-03283
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-09-078-347A-2
Query Match 61.7%; Score 50; DB 4; Length 673;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGCGPP 13
DB 313 LSGRGGCGPP 323

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RESULT 2
US-09-813-819-2
; Sequence 2, Application US/09813819
; Patent No. 6294368
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001177
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-813-819-2

Query Match
Best Local Similarity 60.5%; Score 49; DB 4; Length 855;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLQKPGCGCPP 13
Db 797 KKLQKPGCGCPP 809

RESULT 3
US-09-920-048-2
; Sequence 2, Application US/09920048
; Patent No. 6344352
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: CL001177D1V
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/813,819
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-920-048-2

Query Match
Best Local Similarity 60.5%; Score 49; DB 4; Length 855;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLQKPGCGCPP 13
Db 797 KKLQKPGCGCPP 809

RESULT 4
US-08-709-979A-3
; Sequence 3, Application US/08709979A
; Patent No. 5912157
; GENERAL INFORMATION:
; APPLICANT: Claus von der Osten
; APPLICANT: Martin Sch lein
; TITLE OF INVENTION: No. 5912157el Alkaline Cellulases
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5912157o No. 5912157disk of No. 5912157th America, Inc.
```

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STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,979A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4160,404-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-979A-3

Query Match
Best Local Similarity 55.6%; Score 45; DB 2; Length 402;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KKLQKPGCG-----PPPK 14
Db 42 RAEGLDPGCGGDMGNPPK 60

RESULT 5
US-08-709-974A-1
; Sequence 1, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127v
; REFERENCE/DOCKET NUMBER: 4160,414-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
```

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 93;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14
: | | | | | | | | | |
DB 42 RAEGIGPGCGDHCNPPPK 60

RESULT 6
US-08-709-974A-5
Sequence 5, Application US/08709974A
Patent No. 6117664

GENERAL INFORMATION:
APPLICANT: Sch Jein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
TITLE OF INVENTION: No. 6117664e1 Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160,414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 93;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14
: | | | | | | | | | |
DB 42 RAEGIGPGCGDHCNPPPK 60

RESULT 7

US-08-833-642A-5
Sequence 5, Application US/08833642A
Patent No. 5883066

GENERAL INFORMATION:
APPLICANT: Ivan M. A. J. Herbots et al.
TITLE OF INVENTION: Liquid Detergent Compositions
Containing Cellulase and Amine
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackie Ann Zurcher
ADDRESS: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,642A
FILING DATE: April 8, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A.
REGISTRATION NUMBER: P42,251
REFERENCE/DOCKET NUMBER: CM551C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8377
TELEFAX: (513) 977-8141

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 47.4%; Pred. No. 96;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 2 KLOGKPGG-----PPPK 14
: | | | | | | | | | |
DB 42 RAEGIGPGCGDHCNPPPK 60

RESULT 8
US-08-709-974A-4
Sequence 4, Application US/08709974A
Patent No. 6117664

GENERAL INFORMATION:
APPLICANT: Sch Jein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
TITLE OF INVENTION: No. 6117664e1 Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160,414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-4

Query Match
Best Local Similarity 55.6%; Score 45; DB 3; Length 415;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
OY 2 KLOGKPGG-----PPPK 14
: : | | | | | | | | | |
Db 42 RAEGLGPGGCGDMGNPPK 60

RESULT 9
US-09-069-632-1
Sequence 1, Application US/09069632
Patent No. 6261828
GENERAL INFORMATION:
APPLICANT: Lund, Henrik
TITLE OF INVENTION: A Process For Combined Desizing
TITLE OF INVENTION: And Stone-Washing of Dyed Denim
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,632
FILING DATE: 29-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK96/00469
FILING DATE: 15-NOV-1996
APPLICATION NUMBER: 1278/95
FILING DATE: 15-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4588,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-069-632-1
Query Match
Best Local Similarity 55.6%; Score 45; DB 4; Length 415;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
OY 2 KLOGKPGG-----PPPK 14
: : | | | | | | | | | |
Db 42 RAEGLGPGGCGDMGNPPK 60

RESULT 10
US-08-361-920-27
Sequence 27, Application US/08361920
Patent No. 5457046
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 54570460 No. 5457046disk of No. 5457046th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3435,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-361-920-27

Query Match
Best Local Similarity 55.6%; Score 45; DB 1; Length 435;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
OY 2 KLOGKPGG-----PPPK 14
: : | | | | | | | | | |
Db 62 RAEGLGPGGCGDMGNPPK 80

RESULT 11
US-08-479-939-27

Sequence 27, Application US/08479939
Patent No. 5686593
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479, 939
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361, 920
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 07/940, 860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET INFORMATION: 3435, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-939-27

Query Match 55.6%; Score 45; DB 1; Length 435;
Best Local Similarity 47.4%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
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Db 62 RAEGLGPGCGGDMGNPPK 80

RESULT 12
US-08-483-432-27
Sequence 27, Application US/08483432
Patent No. 5763254
GENERAL INFORMATION:
APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hasstrup
TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
TITLE OF INVENTION: or Hemicellulose
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 57632540 No. 5763254disk of No. 5763254th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483, 432
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361, 920
FILING DATE:
APPLICATION NUMBER: US 07/940, 860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET INFORMATION: 3435, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-432-27

Query Match 55.6%; Score 45; DB 1; Length 435;
Best Local Similarity 47.4%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
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Db 62 RAEGLGPGCGGDMGNPPK 80

RESULT 13
US-09-069-632-3
Sequence 3, Application US/09069632
Patent No. 6261828
GENERAL INFORMATION:
APPLICANT: Lund, Henrik
TITLE OF INVENTION: A Process For Combined Desizing
TITLE OF INVENTION: And Stone-Washing of Dyed Denim
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069, 632
FILING DATE: 29-APR-1998

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Greg9, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

Query Match          55.6%; Score 45; DB 4; Length 435;
Best Local Similarity 47.4%; Pred. No. 1e+02;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

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       : | | | | | | | |
Db      62 RAEGLPGGCGGDMGNPPK 80

RESULT 14
US-09-817-180-2
; Sequence 2, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-2

Query Match          55.6%; Score 45; DB 4; Length 752;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 KLQKGPGRGPP 13
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       : | | | | | | | |
Db      387 KLEHLGPGEPP 398

RESULT 15
US-09-817-180-4
; Sequence 4, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-4

Query Match          55.6%; Score 45; DB 4; Length 822;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 KLQKGPGRGPP 13
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Db      387 KLEHLGPGEPP 398

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Job time : 3.41599 secs
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us-09-821-726a-3.rapb

Mon Apr 14 14:02:40 2003

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model
Run on: April 11, 2003, 16:11:18 ; Search time 1.39315 Seconds
(without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726a-3
Perfect score: 81
Sequence: 1 KKLCKGKGGGPPK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues 248812

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications-AA:*

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- 11: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
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- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	81	100.0	185	9	US-09-992-598-211
3	81	100.0	185	9	US-09-989-293A-211
4	81	100.0	185	9	US-09-989-735-211
5	81	100.0	185	9	US-09-990-444-211
6	81	100.0	185	9	US-10-001-054-14
7	81	100.0	185	9	US-09-989-730-211
8	81	100.0	185	9	US-09-990-436-211
9	81	100.0	185	9	US-09-991-181-211
10	81	100.0	185	9	US-09-993-687-211
11	81	100.0	185	9	US-09-993-653-211
12	81	100.0	185	9	US-09-993-667-211
13	81	100.0	185	9	US-09-990-438-211
14	81	100.0	185	9	US-09-990-562-211
15	81	100.0	185	9	US-09-997-428-211
16	81	100.0	185	9	US-09-997-666-211
17	81	100.0	185	9	US-10-227-884-148
18	81	100.0	185	9	US-09-990-711-211
19	81	100.0	185	9	US-09-990-711-211

20	81	100.0	185	9	US-10-230-163-148	Sequence 148, App
21	81	100.0	185	9	US-09-989-726-211	Sequence 211, App
22	81	100.0	185	9	US-09-746-783-146	Sequence 146, App
23	81	100.0	185	9	US-09-990-437-211	Sequence 211, App
24	81	100.0	185	9	US-09-988-156-211	Sequence 148, App
25	81	100.0	185	9	US-10-218-631-148	Sequence 211, App
26	81	100.0	185	9	US-10-230-338-148	Sequence 211, App
27	81	100.0	185	9	US-09-991-157-211	Sequence 211, App
28	81	100.0	185	9	US-09-991-172-211	Sequence 211, App
29	81	100.0	185	9	US-09-997-573-211	Sequence 211, App
30	81	100.0	185	9	US-09-991-854-211	Sequence 211, App
31	81	100.0	185	9	US-10-230-414-148	Sequence 148, App
32	81	100.0	185	9	US-09-990-443-211	Sequence 211, App
33	81	100.0	185	9	US-09-990-726-211	Sequence 211, App
34	81	100.0	185	9	US-09-997-559-211	Sequence 211, App
35	81	100.0	185	9	US-09-997-601-211	Sequence 211, App
36	81	100.0	185	9	US-09-989-729A-211	Sequence 211, App
37	81	100.0	185	9	US-09-991-854-211	Sequence 211, App
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41	81	100.0	185	9	US-09-997-628-211	Sequence 211, App
42	81	100.0	185	9	US-09-997-683-211	Sequence 211, App
43	81	100.0	185	9	US-09-989-722-211	Sequence 211, App
44	81	100.0	185	10	US-09-989-723-211	Sequence 211, App
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ALIGNMENTS

RESULT 1
US-10-050-704-212
Sequence 212, Application US/10050704
Publication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT FILING DATE: 2002-01-18
PRIORITY FILING DATE: 09/684, 524
PRIORITY APPLICATION NUMBER: 2000-10-10
PRIORITY FILING DATE: 2000-10-10
PRIORITY APPLICATION NUMBER: PCT/US00/08979
PRIORITY FILING DATE: 1999-04-09
PRIORITY APPLICATION NUMBER: 60/128, 693
PRIORITY FILING DATE: 1999-04-26
PRIORITY APPLICATION NUMBER: 60/130, 991
PRIORITY FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 212
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-704-212

Query Match
Best Local Similarity 100.0%; Score 81; DB 9; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-992-598-211
Sequence 211, App
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
Baker, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C20
 CURRENT APPLICATION NUMBER: US/09/992,598
 PRIOR APPLICATION NUMBER: 2001-11-14
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083322
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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-09
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 Best Local Similarity 100.0%; Pred. No. 0.001; 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;

QY 1 KKLCKGCGGPPK 14
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 DB 104 KKLCKGCGGPPK 117

RESULT 3
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 Sequence 211, Application US/09989293A
 Patent No. US2002017164A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerbasi, Hanspeter
 APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoletti, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P27301C66
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: US/09/989, 293A
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
 Best Local Similarity 100.0%; Pred.No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KKLGGKGGGPPK 14
 Db 104 KKLGGKGGGPPK 117

RESULT 4
 US-09-989-735-211
 Sequence 211, Application US/09989735
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;

Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGGPPK 14
 Db 104 KKLGGKGGGPPK 117

RESULT 5

US-09-990-444-211

Sequence 211, Application US/09990444

Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
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 APPLICANT: Gerltzen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C19
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPK 14
Db 104 KKLGGKGGGPPK 117

RESULT 6
US-10-001-054-14
Sequence 14, Application US/10001054
Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
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 ? PRIOR FILING DATE: 2001-08-29
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 ? SEQ ID NO: 14
 ? LENGTH: 185
 ? TYPE: PRT
 ? ORGANISM: Homo Sapien
 US-10-001-054-14

Query Match 100.0%; Score 81; DB 9; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGGPPK 14
 Db 104 KKLGGKGGGPPK 117

RESULT 7
 US-09-989-730-211
 ? Sequence 211, Application US/09989730
 ? Publication No. US20020197674A1

GENERAL INFORMATION:

? APPLICANT: Ashkenazi, Avi J.
 ? APPLICANT: Baker, Kevin P.
 ? APPLICANT: Botstein, David
 ? APPLICANT: Desnovers, Luc
 ? APPLICANT: Eaton, Dan L.
 ? APPLICANT: Ferrara, Napoleone
 ? APPLICANT: Fong, Sherman
 ? APPLICANT: Gerber, Hanspeter
 ? APPLICANT: Gerlitsen, Mary E.
 ? APPLICANT: Goddard, Audrey
 ? APPLICANT: Godowski, Paul J.
 ? APPLICANT: Grimaldi, J. Christopher
 ? APPLICANT: Gurney, Austin L.
 ? APPLICANT: Kljavin, Ivar J.
 ? APPLICANT: Napier, Mary A.
 ? APPLICANT: Pan, James
 ? APPLICANT: Paoni, Nicholas F.
 ? APPLICANT: Roy, Margaret Ann
 ? APPLICANT: Stewart, Timothy A.
 ? APPLICANT: Tumas, Daniel
 ? APPLICANT: Watanabe, Colin K.
 ? APPLICANT: Williams, P. Mickey
 ? APPLICANT: Wood, William I.
 ? APPLICANT: Zhang, Zemin
 ? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ? FILE REFERENCE: P2730PIC69
 ? CURRENT APPLICATION NUMBER: US/09/989,730
 ? CURRENT FILING DATE: 2001-11-20
 ? PRIOR APPLICATION NUMBER: 60/049787
 ? PRIOR FILING DATE: 1997-06-16
 ? PRIOR APPLICATION NUMBER: 60/062250
 ? PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 81; DB 9; Length 185;
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QY 1 KLOGKGPGGPPK 14
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 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
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 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
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 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 KKLGGKGGGPPK 14
DB 104 KKLGGKGGGPPK 117

RESULT 9
US-09-991-181-211
; Sequence 211, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PTC53
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;; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 81; DB 9; Length 185;
Best local similarity 100.0%; Pred. No. 0.001;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKGKGGGPPK 14
DB 104 KKGKGGGPPK 117
RESULT 10
US-09-993-687-211
; Sequence 211, Application US/09993687
; Publication No. US2002019814941
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC11
; CURRENT APPLICATION NUMBER: US/09/993,687
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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 ? PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGPPK 14
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 Db 104 KKLGGKGGPPK 117

RESULT 11
US-09-989-734-211
Sequence 211, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLGGKGGPPK 14
Db 104 KKLGGKGGPPK 117

RESULT 12
US-09-997-653-211
Sequence 211, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Geider, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C38
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
 Best local Similarity 100.0%; Pred. No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPK 14
 Db 104 KKLQKGPGGPPK 117

RESULT 13
 US-09-993-667-211
 ; Sequence 211, Application US/09993667
 ; Publication No. US20030022187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C4
 CURRENT APPLICATION NUMBER: US/09/993,667
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
Best Local Similarity 100.0%; Pred No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLQKGGGPPK 14
Db 104 KKLQKGGGPPK 117

RESULT 14
US-09-990-438-211
; Sequence 211, Application US/09990438
; Publication No. US2003002754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C3
CURRENT APPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2001-11-14
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Query Match 100.0%; Score 81; DB 9; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGGPPK 14
 DB 104 KKLGGKGGGPPK 117

RESULT 15
 US-09-990-562-211
 Sequence 211, Application US/09990562
 Publication No. US20030027965A1
 GENERAL INFORMATION:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC18
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 81; DB 9; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLGGKGGPPPK 14
 |||||
 DB 104 KKLGGKGGPPPK 117

Search completed: April 11, 2003, 16:17:42
 Job time : 2.39315 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 1.50734 Seconds
(without alignments)
892.885 Million cell updates/sec

Title: US-09-821-726a-3
Perfect score: 81
Sequence: 1 KKLCKGPGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	74.1	1677	2 T14267	Xin protein, stage
2	50	61.7	673	1 BVECB	excision nuclease ABC C
3	50	61.7	673	2 A99736	DNA repair, excisi
4	50	61.7	673	2 B85586	excision nuclease
5	50	61.7	673	2 AD0597	hypothetical prote
6	47	58.0	22	2 C42856	hypothetical prote
7	47	58.0	669	2 D82739	excision nuclease ABC s
8	46	56.8	377	2 E87022	probable conserved
9	46	56.8	426	2 A39695	transforming prote
10	46	56.8	551	2 S57447	HPHRII-7 protein -
11	46	56.8	830	2 T16148	hypothetical prote
12	46	56.8	1105	2 S40243	hypothetical prote
13	46	56.8	1215	2 T32734	DNA-directed DNA p
14	46	56.8	1357	2 T29265	myosin-IA - Acanth
15	46	56.2	579	2 D72092	hypothetical prote
16	45.5	56.2	579	2 C86532	conserved hypothet
17	45.5	56.2	579	2 H96833	CT082 hypothetical
18	45	55.6	477	2 TVMVC	hypothetical prote
19	45	55.6	609	1 TVMVC	protein-tyrosine k
20	45	55.6	820	1 TVMVC	protein-tyrosine k
21	45	55.6	820	1 TVMVC	protein-tyrosine k
22	45	55.6	820	1 TVMVC	protein-tyrosine k
23	45	55.6	820	1 TVMVC	protein-tyrosine k
24	44	54.3	142	2 D32880	hypothetical prote
25	44	54.3	149	2 T11446	plastoquinol-plast
26	44	54.3	182	2 B86462	hypothetical prote
27	44	54.3	218	1 TVHURR	transforming prote
28	44	54.3	230	1 TVHURR	nitric-oxide synth
29	44	54.3	347	2 E97487	hypothetical prote

30	44	54.3	347	2 AE2705	ABC transporter, S
31	44	54.3	558	2 B81711	conserved hypothet
32	44	54.3	560	2 D71560	hypothetical prote
33	44	54.3	593	2 D74323	cell division cycl
34	44	54.3	670	2 A83255	excision nuclease ABC s
35	44	54.3	706	2 D97303	ABC-type multidrug
36	44	54.3	996	2 A71080	hypothetical prote
37	44	54.3	1202	2 S71424	nitric-oxide synth
38	44	54.3	1203	1 A47501	nitric-oxide synth
39	44	54.3	1205	1 A38943	nitric-oxide synth
40	44	54.3	1464	2 S59836	collagen alpha 1(I
41	43.5	53.7	1049	1 CG8075	collagen alpha 1(I
42	43	53.1	140	2 S46351	vpx protein - simi
43	43	53.1	189	2 A86369	hypothetical prote
44	43	53.1	221	2 G72665	hypothetical prote
45	43	53.1	224	2 B72710	hypothetical prote

ALIGNMENTS

RESULT 1
T14267
Xin protein, stage early embryo - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
A:Accession: T14267
R:Wang, D.Z.; Lin, J.J.C.
submitted to the EMBL Data Library, March 1998
A:Description: Involvement of a novel gene, Xin, in cardiac looping.
A:Reference number: Z17948
A:Accession: T14267
A:Status: preliminary; translated from GB/EMBL/DBD1
A:Molecule type: mRNA
A:Residues: 1-1677 <NAN>
A:Cross-references: EMBL:AF051945; NID:92970645; PID:92970646; PIDN:AAC06023.1
A:Experimental source: cardiac muscle; stage early embryo

Query Match
Best local similarity 81.8%; Pred. NO. 1.9;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 QGKPGGPPPK 14
DB 574 ECKGPGGPPPE 584

RESULT 2

BVECB
excision nuclease ABC chain B - Escherichia coli (strain K-12)
N:Alternate names: uvrb protein
C:Species: Escherichia coli
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
A:Accession: A93613; A93612; C64814; A23765; A24839
R:Backendorf, C.; Spatnik, H.; Barbelro, A.P.; van de Putte, P.
Nucleic Acids Res. 14, 2877-2890, 1986
A:Title: Structure of the uvrb gene of Escherichia coli. Homology with other DNA repara
A:Reference number: A93613; MUID:8616773; PMID:3008099
A:Accession: A93613
A:Molecule type: DNA
A:Residues: 1-673 <BAC>
A:Cross-references: GB:X03722; NID:943285; PIDN:CAA27357.1; PID:943286
R:Arlikar, E.; Kulkarni, M.S.; Thomas, D.C.; Sancar, A.
Nucleic Acids Res. 14, 2637-2650, 1986
A:Title: Sequences of the E. coli uvrb gene and protein.
A:Reference number: A93612; MUID:8616755; PMID:3515321
A:Accession: A93612
A:Molecule type: DNA
A:Residues: 1-476; R, 478-673 <ARI>
A:Cross-references: GB:X03678; GB:J01722; GB:M24329; GB:V00374; GB:V00375;
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Ferna, N.T.; Burland, V.; Riley, M.;
A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C64814
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-673 <BLAT>
A:Cross-references: GB:AE000180; GB:U00096; NID:q1786988; PIDN:AAC73866.1; PID:q1786996;
C:Comment: Source: strain K-12, substrain MG1655
C:Genetics: uvrA, uvrB, and uvrC function together as excision nuclease.
A:Gene: uvrB
A:Map position: 18 min
C:Function:
A:Description: stimulates the ATPase activity of uvrA protein in the presence of UV-irradiation
C:Superfamily: excinuclease ABC chain B
C:Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop
F:39-46/Region: nucleotide-binding motif A (P-loop)
F:334-339/Region: nucleotide-binding motif B
F:338-341/Region: DEXH motif

Query Match
Best Local Similarity 61.7%; Score 50; DB 1; Length 673;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKPGGPP 13
DB 313 LSGRGPGEPP 323

RESULT 3
A99736
excision nuclease subunit B [Imported] - *Escherichia coli* (strain O157:H7, substrain RIM)
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: A99736
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A99736
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-673 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA834280.1; PID:q13360316; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509552
C:Genetics:
A:Gene: ECS0857
C:Superfamily: excinuclease ABC chain B

Query Match
Best Local Similarity 72.7%; Score 50; DB 2; Length 673;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKPGGPP 13
DB 313 LSGRGPGEPP 323

RESULT 4
B85586
DNA repair, excision nuclease subunit B [Imported] - *Escherichia coli* (strain O157:H7, S)
C:Species: *Escherichia coli*
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85586
R:Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:1120551
A:Accession: B85586
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-673 <STO>
A:Cross-references: GB:AE005174; NID:q12513768; PIDN:AG55150.1; GSPDB:GN00145; UMGF:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: uvrB
C:Superfamily: excinuclease ABC chain B

Query Match
Best Local Similarity 61.7%; Score 50; DB 2; Length 673;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKPGGPP 13
DB 313 LSGRGPGEPP 323

RESULT 5
AD0597
excision nuclease ABC chain B STY0831 [Imported] - *Salmonella enterica* subsp. enteric
C:Species: *Salmonella enterica* subsp. enterica serovar Typh
A:Note: this species has also been called *Salmonella typhi*
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD0597
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se
A:Reference number: AB0502; PMID:11677608
A:Accession: AD0597
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-673 <PAR>
A:Cross-references: GB:AL513382; PIDN:CA005246.1; PID:q16502016; GSPDB:GN00176
A:Genetics:
A:Gene: STY0831
C:Superfamily: excinuclease ABC chain B

Query Match
Best Local Similarity 72.7%; Score 50; DB 2; Length 673;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKPGGPP 13
DB 313 LSGRGPGEPP 323

RESULT 6
C42856
hypothetical protein 3 EPF-region [Imported] - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: C42856
R:Liu, Z.; Diaz, L.A.; Haas, A.L.; Giudice, G.J.
J. Biol. Chem. 267, 15829-15835, 1992
A:Title: cDNA cloning of a novel human ubiquitin carrier protein. An antigenic domain
this human epidermal transcript.
A:Reference number: A42856; MUID:92348449; PMID:1379239
A:Accession: C42856
A:Status: preliminary
A:Molecule type: mRNA
A:Experimental source: keratinocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:109895, NCBIIP:109899)

Query Match
Best Local Similarity 58.0%; Score 47; DB 2; Length 22;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 LOGKPGGPP 13

Mon Apr 14 14:02:42 2003

us-09-821-726a-3.rpt

Db 6 KNAGRGPGCPP 17

RESULT 7

D82739

exinuclease ABC subunit B XF0967 [Imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Accession: D82739

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82739

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-669 <SIM>

A:Cross-references: GB:AE003935; GB:AE003849; NID:g9105894; PIDN:AAF83777.1; GSPDB:GN001

A:Experimental source: Strain 9a5c

R:Stimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carter, R

as-Nevo, E.; Docena, C.; El-Dorfi, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurama, E.F.; Martins, B

Chado, M.A.; Madeira, A.M.N.; Madeira, H.M.F.; Marino, C.L.; Marques, E.C.; Miyaki, C.Y.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Gene: XF0967

C:Superfamily: exinuclease ABC chain B

Query Match

Best Local Similarity 58.0%; Score 47; DB 2; Length 669;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLCKGPGCPP 13

Db 311 RHLGKAPGCPP 323

RESULT 8

E87022

Probable conserved membrane protein ML0907 [Imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87022

R:Colet, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87022

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <STO>

A:Cross-references: GB:AL450380; NID:g13092977; PIDN:CAC31288.1; GSPDB:GN00147

C:Gene: ML0907

Query Match

Best Local Similarity 56.8%; Score 46; DB 2; Length 377;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 GPGGCPP 13

Db 254 GPGGCPP 260

RESULT 9

A39695

transferring protein (N-myc) - common canary

C:Species: Serinus canaria (common canary)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997

C:Accession: A39695

R:Collum, R.G.; Clayton, D.F.; Alt, F.W.

Mol. Cell. Biol. 11, 1770-1776, 1991

A:Title: Structure and expression of canary myc family genes.

A:Reference number: A39695; MUID:9114534; PMID:1996121

A:Accession: A39695

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-426 <COL>

A:Cross-references: GB:M64251; GB:M64598

C:Superfamily: myc transforming protein; myc transforming protein homology

C:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein

F:11-426/Domain: myc transforming protein homology motif

F:395-423/Region: leucine zipper motif

Query Match

Best Local Similarity 56.8%; Score 46; DB 2; Length 426;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLCKGPGCPP 13

Db 144 EKLNKTPAAPP 156

RESULT 10

S57447

HPR11-7 protein - human

N:Alternate names: HPR11-4 protein

C:Species: Homo sapiens (man)

C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C:Accession: S57447; S57489

R:Flerschauer, K.L.

submitted to the EMBL Data Library, June 1992

A:Reference number: S57447

A:Accession: S57447

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-551 <FLD>

A:Cross-references: EMBL:X67336; NID:g871300; PIDN:CAA47752.1; PID:g871301

A:Accession: S57489

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FLD>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

A:Accession: S57489

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FLD>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

A:Accession: S57489

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FLD>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

A:Accession: S57489

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FLD>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

A:Accession: S57489

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FLD>

Page 3

R:Taich, A.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of C. elegans cosmid F25B5.
 A:Reference number: 218468
 A:Accession: T16148
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-561 <TAI>
 A:Cross-references: EMBL:U23172; NID:g726388; PID:g726394; PIDN:AAC46528.1; CESP:F25B5.7
 A:Experimental source: strain Bristol N2
 A:Gene: CESP:F25B5.7
 A:Introns: 39/2; 157/3; 258/2; 290/2; 356/1; 531/1

Query Match
 Best Local Similarity 56.8%; Score 46; DB 2; Length 561;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 GPGGPPP 13
 Db 409 GPGGPPP 415

RESULT 12
 T18860
 hypothetical protein CO2C6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T18860
 R:Swindburn, J.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: 219032
 A:Accession: T18860
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-830 <WIL>
 A:Cross-references: EMBL:Z79596; PIDN:CAB01857.1; GSPDB:GN00028; CESP:CO2C6.1
 A:Experimental source: clone CO2C6
 A:Gene: CESP:CO2C6.1
 A:Map position: X
 A:Introns: 56/2; 131/1; 333/2; 501/2; 593/2; 686/3; 815/2
 C:Superfamily: human dynamin II; pleckstrin repeat homology

Query Match
 Best Local Similarity 56.8%; Score 46; DB 2; Length 830;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 GPGGPPP 13
 Db 818 GPGGPPP 824

RESULT 13
 S40243
 DNA-directed DNA polymerase (EC 2.7.7.7) delta chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S40243; J06670
 R:Cullmann, G.; Hindges, R.; Berchtold, M.W.; Huebscher, U.
 submitted to the EMBL Data Library, March 1993
 A:Reference number: S40243
 A:Accession: S40243
 A:Molecule type: mRNA
 A:Residues: 1-1105 <CU>
 A:Cross-references: EMBL:221848; NID:g438133; PIDN:CAA7895.1; PID:g438134
 Gene 134, 191-200, 1993
 A:Title: Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of the homolo
 A:Reference number: J06670; MUID:94085777; PMID:8262377
 A:Molecule type: DNA
 A:Residues: 1-111, 'G', 113, 'P', 115-1034, 'Y', 1036-1105 <CU>

A:Cross-references: EMBL:221848
 A:Note: the sequence translated from 221848 is inconsistent with that from this sequ
 C:Comment: Three DNA polymerases alpha, delta and epsilon chains are essential. This
 C:Genetics: poldelta
 A:Gene: poldelta
 C:Superfamily: herpesvirus DNA-directed DNA polymerase
 C:Keywords: DNA replication; heterodimer; nucleotidyltransferase

Query Match
 Best Local Similarity 56.8%; Score 46; DB 1; Length 1105;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 KKGKGGGPPK 14
 Db 4 KRGGGPPGVPKR 17

RESULT 14
 T32734
 myosin-1A - Acanthamoeba castellanii
 C:Species: Acanthamoeba castellanii
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
 C:Accession: T32734
 R:Lee, W.L.; Ostap, E.M.; Zol, H.G.; Pollard, T.D.
 submitted to the EMBL Data Library, August 1998
 A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-1A G
 A:Reference number: 221216
 A:Accession: T32734
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1215 <LE>
 A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1
 A:Experimental source: strain Neff
 A:Gene: MYA
 A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 5
 C:Superfamily: protozoan myosin heavy chain 1b; myosin motor domain homology; SH3 hom
 F:14-674/Domain: myosin motor domain homology <MMO>

Query Match
 Best Local Similarity 56.8%; Score 46; DB 2; Length 1215;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 GPGGPPP 13
 Db 1075 GPGGPPP 1081

RESULT 15
 T29265
 hypothetical protein C01G8.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T29265
 R:Du, Z.; Gatlung, S.
 submitted to the EMBL Data Library, November 1996
 A:Description: The sequence of C. elegans cosmid C01G8.
 A:Reference number: Z20597
 A:Accession: T29265
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1357 <DD>
 A:Cross-references: EMBL:U80439; PIDN:AA837645.1; GSPDB:GN00019; CESP:C01G8.7
 A:Experimental source: strain Bristol N2; clone C01G8
 A:Gene: CESP:C01G8.7
 A:Map position: 1
 A:Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3

Query Match
 Best Local Similarity 56.8%; Score 46; DB 2; Length 1357;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	7	GP	GP	GP	GP	13
Db	153	GP	GP	GP	GP	159

Search completed: April 11, 2003, 16:15:28
Job time : 3.50734 secs

Mon Apr 14 14:02:52 2003

us-09-821-726a-3.ispt

Page 1

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model
Run on: April 11, 2003, 16:07:33 ; Search time 3.10604 Seconds
(without alignments)
928.727 Million cell updates/sec

Title: US-09-821-726A-3
Perfect score: 1 KKLGGKPGGPPPK 14
Sequence: BLASTUM62
Scoring table: Gapop 10.0, Capext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mmc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-unclassified:*
14: SP-virus:*
15: SP-bacteriophage:*
16: SP-bacteriophage:*
17: SP-archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	74.1	1677	11 070373	070373 mus musculus
2	52	64.2	467	11 09H9F1	09H9F1 homo sapien
3	50	61.7	333	2 09APQ3	09APQ3 unclutered
4	49	60.5	212	2 09APJ1	09APJ1 methylolact
5	48	59.3	409	16 08XRL2	08XRL2 raltstonia s
6	48	59.3	547	11 097472	097472 mus musculu
7	48	59.3	774	5 09V620	09V620 mus musculu
8	48	59.3	813	5 095RY2	095RY2 dirosophila
9	48	59.3	1289	10 09PFI07	09PFI07 aradidopsis
10	48	59.3	1292	3 096WLO	096WLO ustillago me
11	48	59.3	2061	3 09V0H9	09V0H9 dirosophila
12	47	58.0	104	6 08WNT3	08WNT3 procyon lot
13	47	58.0	262	12 09DMB2	09DMB2 rat clyomeg
14	47	58.0	420	4 08WYU4	08WYU4 homo sapien
15	47	58.0	494	6 08S068	08S068 sus scrofa
16	47	58.0	494	6 08S068	08S068 sus scrofa

17	47	58.0	673	2 09RBK2	09RBK2 xanthomonas
18	47	58.0	1963	5 09VSK5	09VSK5 dirosophila
19	47	58.0	1966	5 09NHX6	09NHX6 dirosophila
20	47	58.0	1985	5 08T9N4	08T9N4 oryza sativ
21	46	56.8	172	10 08S0G1	08S0G1 homo sapien
22	46	56.8	241	4 095542	095542 homo sapien
23	46	56.8	250	4 075894	075894 caenorhabdi
24	46	56.8	281	5 095010	095010 caenorhabdi
25	46	56.8	322	13 09P1B4	09P1B4 mycobacteri
26	46	56.8	377	16 069559	069559 caenorhabdi
27	46	56.8	495	5 095YB0	095YB0 homo sapien
28	46	56.8	549	5 09B1B7	09B1B7 caenorhabdi
29	46	56.8	551	4 016630	016630 caenorhabdi
30	46	56.8	561	4 009542	009542 caenorhabdi
31	46	56.8	588	4 09BWI8	09BWI8 homo sapien
32	46	56.8	1105	11 091V70	091V70 mus musculu
33	46	56.8	1194	5 09M485	09M485 dirosophila
34	46	56.8	1215	5 077202	077202 acanthamoeb
35	46	56.8	1256	5 095YV9	095YV9 caenorhabdi
36	46	56.8	1284	5 0960F1	0960F1 dirosophila
37	46	56.8	1724	5 091019	091019 caenorhabdi
38	46	56.2	579	16 0928K7	0928K7 chlamydia p
39	45	55.0	153	11 09CTM4	09CTM4 mus musculu
40	45	55.6	171	10 09S8B8	09S8B8 oryza sativ
41	45	55.6	224	10 08R238	08R238 chimpanzee
42	45	55.6	316	15 099857	099857 chimpanzee
43	45	55.6	497	10 08S1B7	08S1B7 oryza sativ
44	45	55.6	585	4 08TE04	08TE04 homo sapien
45	45	55.6	976	6 09M2T1	09M2T1 canis famli

ALIGNMENTS

RESULT 1

070373 PRELIMINARY: PRT: 1677 AA.

AC 070373: 070373: 07, Created)
DT 01-AUG-1998 (TRENBERG, 07, last sequence update)
DT 01-AUG-1998 (TRENBERG, 07, last sequence update)
DT 01-DEC-2001 (TRENBERG, 19, last annotation update)
DE Xin.
GN Xin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed=9159189;
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;
RT "differential display of mRNAs from the atrioventricular region of
developing chicken hearts at stages 15 and 21.";
RT Front. Biosci. 1:1-15(1996).
RU [2]

RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed=9159189; PubMed=10021346;
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,
Krob S.L., Schulteis T.M., Evans S., Lin J.J.-C.;
RT "Requirement of a novel gene, Xin, in cardiac morphogenesis.";
EMBL: AF01945; AAC06023.1; -;
DR MGI: MGI:133878; Xin.
SQ SEQUENCE 1677 AA; 182085 MW; A201CFGA710CTFF CRC64;
Query Match 74.1%; Score 60; DB 11; Length 1677;
Best local Similarity 81.8%; Pred. No. 2.2;
Matches 9; Conservative 0; Indels 0; Gaps 0;

Db 574 ECKGPGGPPPE 584

RESULT 2

Q9H9F1

ID Q9H9F1

PRELIMINARY;

PRT; 467 AA.

AC Q9H9F1

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-JUN-2001 (TREMBLrel. 16, Last sequence update)

DE CDNA FLJ12800 fis, clone NT2RP2002079, weakly similar to histone H1, gonadal.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.

RN NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

RA Arita M., Nebekura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

RA Wakamatsu A., Nakamura Y., Ishii S., Kawai Y., Saito K., Yamamoto J.,

RT "NEDO human cDNA sequencing project."

RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AK022862; BAB14278.1; "

DR InterPro: IPR000637; AT_hook.

DR SMART: SM00384; AT_hook.1.

SO SEQUENCE 467 AA; 49648 MW; 287B1BF4CF30B1A1 CRC64;

Query Match

Best Local Similarity 64.2%; Score 52; DB 4; Length 467;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKLGGKPGGPPK 14

Db 213 FKSSGKGPENPPK 226

QY 1 KKLGGKPGGPPK 14

Db 213 FKSSGKGPENPPK 226

RESULT 3

Q9APQ3

ID Q9APQ3

PRELIMINARY;

PRT; 333 AA.

AC Q9APQ3

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE Excision nuclease subunit B (Fragment).

GN UVRB

OS uncultured bacterium pCosHE1.

OC Bacteria; environmental samples.

OX NCBI_TaxID=143796;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20575196; PubMed=11133432;

RA "Direct cloning from enrichment cultures a reliable strategy for

RT isolation of complete operons and genes from microbial consortia."

RL Appl. Environ. Microbiol. 67:89-99(2001).

DR EMBL: AF250772; AAC60567.1; "

DR HSPB; P56981; ID9X.

DR InterPro: IPR001410; DEAD.

FT NON_TER

FT NON_TER

SO SEQUENCE 333 AA; 38155 MW; E6401C01A8A46DEF CRC64;

Query Match

Best Local Similarity 61.7%; Score 50; DB 2; Length 333;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPK 13

Db 135 LSGRGGPPK 145

QY 3 LOGKGGGPPK 13

Db 135 LSGRGGPPK 145

RESULT 4

Q9APJ1

ID Q9APJ1

PRELIMINARY;

PRT; 212 AA.

AC Q9APJ1

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE putative regulator for granula-associated protein.

OC Bacteria; Proteobacteria; alpha subphylum; Rhizobiaceae group;

OC Methylobacterium group; Methylobacterium.

OX NCBI_TaxID=408;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AM1;

RX MEDLINE=21142531; PubMed=11208803;

RA Korotkova N., Lidstrom M.E.;

RT "Connection between Poly-beta-Hydroxybutyrate Biosynthesis and Growth

on C1 and C2 compounds in the Methylobacterium Methylobacterium extorquens

RL J. Bacteriol. 183:1038-1046(2001).

DR EMBL: AF287907; AAK11535.1;

SO SEQUENCE 212 AA; 23141 MW; 4121BD0E8A3FBAC3 CRC64;

Query Match

Best Local Similarity 60.5%; Score 49; DB 2; Length 212;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKGPGGPPK 13

Db 162 GKGPGGPPK 170

QY 5 GKGPGGPPK 13

Db 162 GKGPGGPPK 170

RESULT 5

Q8XRL2

ID Q8XRL2

PRELIMINARY;

PRT; 409 AA.

AC Q8XRL2

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE Probable drug efflux lipoprotein.

GN RSP0819 OR RS01888.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OG Bacteria; Proteobacteria; beta subphylum; Ralstonia group;

OC Bacteria; Proteobacteria; beta subphylum; Ralstonia group;

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GMT1000;

RX MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brothier P., Camus J.C., Cartolico L.,

RA Chandler M., Choinse N., Claudel-Renard C., Cunac S., Demange N.,

RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum."

RL Nature 415:497-502(2002).

DR EMBL: AL646081; CAD17970.1;

DR InterPro: IPR002215; HlyD.

DR Pfam: PF00529; HlyD.

KW plasmid; Complete proteome.

SO SEQUENCE 409 AA; 42873 MW; 97003B2B7F95401B CRC64;

Query Match

Best Local Similarity 60.5%; Score 49; DB 16; Length 409;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKGPGGPPK 13

Db 25 GKGPGGPPK 33

QY 5 GKGPGGPPK 13

Db 25 GKGPGGPPK 33

```

DR PROSITE, PS50023: LIM_DOMAIN.2: 3:
RM LIM domain: Metal-binding: Zinc:
SQ SEQUENCE 547 AA: 57919 MW: C326772AC1C155B2 CRC64:
Query Match 59.3%; Score 48; DB 11; Length 547;
Best Local Similarity 53.8%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0
OY 1 KKLQKGGCGPPP 13
   : : : : :
Db 93 QRFESFGCGPPP 105

RESULT 8
O9V620 PRELIMINARY; PRT: 774 AA.
ID O9V620:
DT 01-MAY-2000 (TRIMBLrel. 13, Created)
DT 01-MAY-2000 (TRIMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
DE CG8991 protein.
OS CG8991.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
   (1)
RX SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RM MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blasei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agayari A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailes R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Berens P.V., Bernier B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A.L., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Foster C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattlei B., McIntosh T.C., McInerney C., Morris J., Moshrefi A.,
RA Mirkulov G., Mishina N.V., Mobarry C., Moritz J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy C., Nusskern D.R., Pacleby J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T.,
RA Spletter R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
   "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003824: AAF5619.1: -
DR FlyBase: FBgn0033654: CG8991.
DR InterPro: IPR002965: P_rich_extensn.
DR PRINTS: PR01217: PRTCHEXTENSN.

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Query Match	59.3%;	Score 48;	DB 5;	Length 774;
Best Local Similarity	61.5%;	Pred. No. 58;		
Matches	8;	Conservative	1;	Mismatches 4.

QY	1	KRLQKGGPGGPPP	13
	:		
Db	366	QKSPGPGPGAPPP	378

ZTC

ID	PRELIMINARY:	PRJ:	813 AA.
IO	0951Y2;		
IT	0951Y2;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	GH22790p.		
GN	CG8991.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OX	Ephyridiidae; Drosophilidae; Drosophila.		
RN	NCBI_TaxID=7227;		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RA	STRAIN=BERKELEY;		
RA	Stapleton M., Broksstein P., Hong L., Abhayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,		
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,		
RA	Nunoo J., Paolel J., Pargacs V., Park S., Phouanavong S., Wan K.,		
RL	Yu C., Lewis S.E., Rubin G.M., Celisner S.;		
DR	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
SO	EMBL: AY058443; AAL13673.1; -		
DR	FlyBase; Bgn0033654; CG8991.		
SO	SEQUENCE 813 AA; 88199 MW; 9B9E9571EA08308C CRC64;		

	Query Match	Best Local Similarity	Matches	Score 48;	DB 5;	Length 813;
		61.5%;		Pred. No. 61;		
		Conservative	1;	Mismatches	4;	Indels
					0;	Gaps
OY	1	KKLOCKGGGCGPP	13			
		:				
Db	405	OKSPGGGGAPP	417			

ID	PRELIMINARY;	PRT;	1289	AA..
Q9FLQ7				
Q9FLQ7;				
AC				

DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE CblIAD23008.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RL physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54(1998).
DR EMBL; AB010070; BAB11454.1; -;
DR InterPro: IPR002965; P_Rich_extensn.
DR PRINTS; PR01582; KV33CHANNEL.

DR PRINTS; PRO1217; PRICEXTENS.
SQ SEQUENCE 1289 AA; 137558 MW; 898E55A2A618F5E0 CRC64;

QY	5	GRSGGPP	13
	1	1	1
	1	1	1
Db	1142	GRSGAPP	1150

Q JOWLE
ID OCT 6

ID Q96WL0: PRELIMINARY: PRT; 1292 AA.
 AC 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE TPR-containing protein Mqll.
 GN Mqll.
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginaceae; Ustilago.
 NCBI_TaxID=5270;
 [1]
 SEQUENCE FROM N.A.
 RA Loubradou G., Kahmann R.
 RT "Involvement of the TPR containing protein Mqll in filamentous growth of Ustilago maydis."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 EMBL: APZ68097; AAK5576.1; -
 JF Interpro: IPR001440; TPR.
 Pfam: PF00515; TPR; 10.
 SEQUENCE 1292 AA; 135886 MW; 543A2702C4ED0610 CRC64;

	59.3%;	Score 48;	DB 3;	Length 1292;
Query March	Best Local Similarity 72.7%;			
Matches	8; Conservative	0; Mismatches	3; Indels	0; Gaps
y	3	LOGKPGCGPP	13	
b	716	LAAGPGCGPP	726	

PRELIMINARY; PRT; 2061 AA

DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE CG9425 protein.
 GN CG9425.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridioidae; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY:
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Holt R.A., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck Y., Brokstein P., Brottlie P.,

[illegible]

RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF318356; AAL55863.1; -;
DR InterPro: IPR000822; Znf_C2H2.
DR Pfam: PF00096; Zf-C2H2; 6.
DR PRINTS: PR00048; ZINC_FINGER.
DR SMART: SM00355; znf_C2H2; 6.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_6.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 6.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 45771 MW; CB01FC26A489060C CRC64;

Query Match 58.0%; Score 47; DB 4; Length 420;
Best Local Similarity 58.3%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKLQCKGPGGP 12
||: : |||||
Db 195 KKIKAKNPGGP 206

Search completed: April 11, 2003, 16:14:17
Job time : 5.10604 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 0.822186 Seconds
(without alignments)
706.250 Million cell updates/sec

Title: US-09-821-726A-3
Perfect score: 81
Sequence: 1 KKLQKGGPGGPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	81	100.0	199	1	CLIP_HUMAN
2	59	72.8	184	1	CLIP_MOUSE
3	50	61.7	673	1	UVRB_ECOLI
4	50	61.7	673	1	UVRB_SALTI
5	48	59.3	532	1	UVRB_SALTY
6	47	58.0	669	1	UVRB_XYLFA
7	46	56.8	427	1	MYCN_SERCA
8	46	56.8	830	1	DYNL_CAEEL
9	46	56.8	1103	1	DPOD_MESAU
10	46	56.8	1103	1	DPOD_MOUSE
11	46	56.8	1105	1	GUNI_HUMIN
12	45	55.6	402	1	FES_FSVST
13	45	55.6	477	1	FES_FSVST
14	45	55.6	609	1	FES_FSVST
15	45	55.6	820	1	FES_FELCA
16	45	55.6	820	1	FES_FELCA
17	44.5	54.9	459	1	RN25_HUMAN
18	44	54.3	142	1	YRUB_KLEPN
19	44	54.3	218	1	RRAS_HUMAN
20	44	54.3	593	1	CC23_SCHPO
21	44	54.3	670	1	UVRB_PSEAE
22	44	54.3	919	1	NOS3_RAT
23	44	54.3	1048	1	AGOL_ARATH
24	44	54.3	1201	1	NOS3_MOUSE
25	44	54.3	1202	1	NOS3_HUMAN
26	44	54.3	1204	1	NOS3_BOVIN
27	44	54.3	1204	1	NOS3_PIG
28	44	54.3	1464	1	CA13_MOUSE
29	43.5	53.1	1049	1	CA13_BOVIN
30	43	53.1	233	1	HB2A_RAT
31	43	53.1	252	1	CRB1_BOVIN
32	43	53.1	252	1	HB2F_MOUSE
33	43	53.1	263	1	HB2B_RAT

34	43	53.1	263	1	HB2K_MOUSE
35	43	53.1	263	1	HB2S_MOUSE
36	43	53.1	263	1	HB2U_MOUSE
37	43	53.1	265	1	HB2D_MOUSE
38	43	53.1	265	1	HB2D_MOUSE
39	43	53.1	268	1	HB2X_HUMAN
40	43	53.1	360	1	OC3A_HUMAN
41	43	53.1	379	1	V671_CHLMU
42	43	53.1	423	1	TVB2_CAEEL
43	43	53.1	736	1	DVL2_MOUSE
44	43	53.1	860	1	ELS_MOUSE
45	43	53.1	860	1	ELS_MOUSE

ALIGNMENTS

RESULT 1

CLIP_HUMAN STANDARD: PRT: 199 AA.

ID CLIP_HUMAN
AC Q9NS71;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CALL protein.
GN CALL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y, Mukai H, Hino F, Asada K, Kato I;
RT Jpn. J. Cancer Res. 91:459-463(2000).
RT *Isolation of two novel genes, down-regulated in gastric cancer.*
CC Jpn. J. Cancer Res. 91:459-463(2000).
CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is
detected in cancer tissue or gastric cancer cell lines.

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CC EMBL: AB039886; BAA92433.1; -;
DR MIM: 606402; -;
DK MIM: 606402; -;
SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;

Query Match 100.0%; Score 81; DB 1; Length 199;
Best local similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLQKGGPGGPPK 14
Db 118 KKLQKGGPGGPPK 131

RESULT 2

CLIP_MOUSE STANDARD: PRT: 184 AA.

ID CLIP_MOUSE
AC Q9CR36; Q9D7K7; Q9CT25;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CALL protein homology.
GN CALL
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

RA MEDLINE=86176773; PubMed=3008099;
RA Backendorf C., Spalk H., Barbiero A.P., van de Putte P.;
RT "Structure of the *uvrB* gene of *Escherichia coli*. Homology with other
RT DNA repair enzymes and characterization of the *uvrB5* mutation.";
RL Nucleic Acids Res. 14:2877-2890(1986).
RN [2]
RN SEQUENCE FROM N.A.
RA MEDLINE=86176755; PubMed=3515321;
RA Arifan E., Kulikarni M.S., Thomas D.C., Sancar A.;
RT "Sequences of the E. coli *uvrB* gene and protein.";
RL Nucleic Acids Res. 14:2637-2650(1986).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RA MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobcek E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.;
RT "Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / K1MD 0509952;
RA MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Tida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [6]
RN SEQUENCE OF 168-673 FROM N.A.
RC STRAIN=K12;
RA MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alpa H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K.,
RA Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S.,
RA Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
RA Nishimoto H., Nishio Y., Saito N., Sempel G., Seki Y., Tagami H.,
RA Takemoto K., Wada C., Yamamoto Y., Yano M., Horikuchi H.,
RA "A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 619-673.
RA MEDLINE=20123894; PubMed=10611336;
RA Sohi M., Alexandrovich A., Moolenaar G., Visse R., Goosen N.,
RA Verneke X., Fontecilla-Camps J.C., Champness J., Sanderson M.R.;
RT "Crystal structure of *Escherichia coli* *uvrB* C-terminal domain, and a
RL model for *uvrB*-*uvrC* interaction.";
RN FEBS Lett. 465:161-164(2000).
RN [8]
RN STRUCTURE BY NMR OF 619-673
RA MEDLINE=99297571; PubMed=10371161;
RA Alexandrovich A., Sanderson M.R., Moolenaar G.F., Goosen N.,
RA Lane A.N.;
RT "NMR assignments and secondary structure of the *uvrB* binding domain of
RT *uvrB*.";
RL FEBS Lett. 451:181-185(1999).

```

CC -1- FUNCTION: THE ABC EXCISION NUCLEASE IS A DNA REPAIR ENZYME THAT
CC CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS
CC PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRB STIMULATES
CC THE ATPase ACTIVITY OF UVRB IN THE PRESENCE OF UV-IRRADIATED
CC DOUBLE-STRANDED DNA. IT ALSO ENHANCES THE ABILITY OF UVRB TO BIND
CC TO UV-IRRADIATED DUPLEX DNA.
CC -1- SUBUNIT: CONSISTS OF THREE SUBUNITS: UVRB, UVRB AND UVRB.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.
CC -1- SIMILARITY: CONTAINS 1 UVR DOMAIN.
-----
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-----
DR EMBL: X03722; CAA27357.1; -
DR EMBL: X03678; CAA27314.1; -
DR EMBL: AE000180; AAC73866.1; -
DR EMBL: AE005259; AAG55150.1; -
DR EMBL: AP002553; BAB34280.1; -
DR EMBL: D90716; BAA35437.1; -
DR PIR: A23765; BVCCUB.
DR PDB: 100J; 10-NOV-00.
DR PDB: 1ES2; 12-JUL-01.
DR ECO2DBASE: C080.0; 6TH EDITION.
DR Ecogene: EGI1062; UVRB.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004807; UVRB.
DR InterPro: IPR001943; UVRB/C.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF02151; UVR; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR TIGRFAMs: TIGR00631; uvrB; 1.
DR PROSITE: PS50151; UVR; 1.
DR SOS response: Excision nuclease; DNA repair; ATP-binding;
KW 3D-structure; Complete proteome.
KM NP_BIND 39 46 ATP (POTENTIAL).
FT DOMAIN 633 668 UVR.
FT SITE 630 631 CLEAVAGE.
FT CONFLICT 477 477 H -> R (IN REF. 2).
SQ SEQUENCE 673 AA; 76226 MW; 2F172045344FDAD7 CRC64;
Query Match 61.7%; Score 50; DB 1; Length 673;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 3 LOGKPGCGPPP 13
DB 313 LSGRGPCEPPP 323

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RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Cornerton P.,
RA Crofton A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hen T.T., Holroyd S., Jacobs K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RU Nature 413:848-852(2001).
CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that
CC catalyzes the excision reaction of UV-damaged nucleotide segments
CC producing oligomers having the modified base(s). UVRB stimulates
CC the ATPase activity of UVRB in the presence of UV-irradiated
CC double-stranded DNA. It also enhances the ability of UVRB to bind
CC to UV-irradiated duplex DNA (By similarity).
CC -1- SUBUNIT: Consists of three subunits: uvrB, uvrB and uvrB.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AL627268; CAD05246.1; -
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004807; UVRB.
DR InterPro: IPR001943; UVRB/C.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF02151; UVR; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR TIGRFAMs: TIGR00631; uvrB; 1.
DR PROSITE: PS50151; UVR; 1.
DR SOS response: Excision nuclease; DNA repair; ATP-binding;
KW Complete proteome.
KM NP_BIND 39 46 ATP (POTENTIAL).
FT DOMAIN 633 668 UVR.
FT SITE 630 631 CLEAVAGE.
FT CONFLICT 477 477 H -> R (IN REF. 2).
SQ SEQUENCE 673 AA; 76206 MW; 0618153FADAC890 CRC64;
Query Match 61.7%; Score 50; DB 1; Length 673;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 3 LOGKPGCGPPP 13
DB 313 LSGRGPCEPPP 323

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RESULT 4
UVRB_SALTY
ID UVRB_SALTY STANDARD: PRT; 673 AA.
AC 082889;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exonuclease ABC subunit B.
GN UVRB OR STY0831.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN NCBI_TaxID=601;
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;

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RESULT 5
UVRB_SALTY
ID UVRB_SALTY STANDARD: PRT; 673 AA.
AC 082004;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exonuclease ABC subunit B.
GN UVRB OR STY0798.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN NCBI_TaxID=602;
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SCS1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RX MEDLINE=21534948; PubMed=11677609;

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RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Portolick S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewel N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that
 CC catalyzes the excision reaction of UV-damaged nucleotide segments
 CC producing oligomers having the modified base(S). UVRB stimulates
 CC the Appase activity of UVRa in the presence of UV-irradiated
 CC double-stranded DNA. It also enhances the ability of UVRa to bind
 CC to UV-irradiated duplex DNA (by similarity).
 CC -1- SUBUNIT: Consists of three subunits; UVRa, UVRB and UVRC.
 CC -1- SIMILARITY: BELONGS TO THE UVRB FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE008733; AAL19735.1; -
 DR StyGene: SG27272; UVRB.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR004807; UVRB.
 DR InterPro: IPR001943; UVRB/C.
 DR Pfam: PF00271; helicase_C; 1.
 DR Pfam: PF02151; UVR; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR TIGRfams: TIGR00631; uvrB; 1.
 DR PROSITE: PS50151; UVR; 1.
 DR SOS response: Excision nuclease; DNA repair; ATP-binding;
 KM Complete proteome.
 KW NP_BIND 39 ATP (POTENTIAL).
 FT DOMAIN 633 668 UVR.
 FT SEQUENCE 673 AA; 76134 MW; 054E205FADA6C890 CRC64;
 SO

Query Match 61.7%; Score 50; DB 1; Length 673;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 3 LOGKGGGPP 13
 DB 313 LSGRGGPP 323

RESULT 6
 CG48_HUMAN
 ID CG48_HUMAN STANDARD; PRT; 532 AA.
 AC 09Y5J1: 09H4N6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical WD-repeat protein CG1-48.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20272150; PubMed=10810093;
 RA Lai C.-H., Chou C.-Y., Chang L.-Y., Lin C.-S., Lin W.-C.;
 RT "Identification of novel human genes evolutionarily conserved in
 RT *Caenorhabditis elegans* by comparative proteomics.";
 RL Genome Res. 10:703-713(2000).
 RN [2]

RP SEQUENCE OF 138-532 FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 6 WD REPEATS (TTP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE CG1-48 FAMILY OF WD-REPEAT PROTEINS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF151806; AAD34043.1; -
 DR EMBL: AY007138; AAG01999.1; ALT_INT.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 8.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00678; WD_REPEATS_1; 1.
 DR PROSITE: PS50082; WD_REPEATS_2; 1.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 DR Hypothetical protein; Repeat; WD repeat.
 FT REPEAT 225 264 WD 1.
 FT REPEAT 269 309 WD 2.
 FT REPEAT 315 356 WD 3.
 FT REPEAT 357 395 WD 4.
 FT REPEAT 397 438 WD 5.
 FT REPEAT 447 488 WD 6.
 FT REPEAT 519 532 WD 6.
 FT SEQUENCE 532 AA; 59103 MW; 2DA86FDF5DF7A1 CMC64;
 SO

Query Match 59.3%; Score 48; DB 1; Length 532;
 Best Local Similarity 80.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 GKGPGGPP 14
 DB 8 GAGPGGPP 17

RESULT 7
 UVRB_XYLFA
 ID UVRB_XYLFA STANDARD; PRT; 669 AA.
 AC 09PER1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Excision nuclease ABC subunit B.
 GN UVRB OR XP0967.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OX Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarado R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto F., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Fromme M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.P., Matsukuma A.Y.,

RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Verjovski-Almeida S., Vettore A.L.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."
 RL Nature 406:151-159(2000).
 CC -1- FUNCTION: The ABC excision nuclease is a DNA repair enzyme that
 CC catalyzes the excision reaction of UV-damaged nucleotide segments
 CC producing oligomers having the modified base(s). UVB stimulates
 CC the ATPase activity of uvra in the presence of UV-irradiated
 CC double-stranded DNA. It also enhances the ability of uvra to bind
 CC to UV-irradiated duplex DNA (by similarity).
 CC -1- SUBUNIT: Consists of three subunits; uvra, uvrb and uvrc.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE UVB FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 UVR DOMAIN.
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 CC
 CC EMBL: AE003935; AAF8377.1; -
 DR HSSP: P56981; 1D9X.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR004807; UVRB.
 DR InterPro: IPR001943; UVRB/EC.
 DR InterPro: PF00271; helicase_C; 1.
 DR Pfam: PF02151; UVR; 1.
 DR SMART: SM00487; DEHC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR TIGRfam: TIGR00631; uvrb; 1.
 DR PROSITE: PS50151; UVR; 1.
 KM SOS response: Excision nuclease; DNA repair; ATP-binding;
 KM Complete proteome.
 FT NP_BIND 39 46 ATP (POTENTIAL).
 FT DOMAIN 631 666 UVR
 SQ SEQUENCE 669 AA; 75557 MW; 26BA460383A7125E CRC64;
 Query Match 58.0%; Score 47; DB 1; Length 669;
 Best Local Similarity 61.5%; Pred. No. 28;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLQKGGPGGPP 13
 DB 311 RHLTGKAPGPP 323
 RESULT 8
 MYCN_SERCA STANDARD; PRT; 427 AA.
 ID MYCN_SERCA
 AC P26014;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE N-myc proto-oncogene protein.
 GN MYCN.
 OS Serinus canaria (Canary).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Aves; Neognathae; Passeriformes; Passeroidea;
 OC Fringillidae; Carduelinae; Serinus.

OX NCBI_Taxid=9135;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9114534; PubMed=1996121;
 RA Collum R.G., Clayton D.F., Alt F.W.;
 RT "Structure and expression of canary myc family genes."
 RL Mol. Cell. Biol. 11:1770-1776(1991).
 CC -1- SUBUNIT: EFFICIENT DNA BINDING. REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHLH-2IP SUBFAMILY.
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 CC
 CC EMBL: M64598; AAA49540.1; -
 DR EMBL: M64251; AAA49540.1; JOINED.
 DR PIR: A39695; A39695.
 DR HSSP: P25912; 1HL0.
 DR TRANSFAC: T02381; -
 DR InterPro: IPR001092; HLH_basic.
 DR InterPro: IPR002418; TF_Myc.
 DR Pfam: PF00010; HLH; 1.
 DR Pfam: PF01056; MYC_N-term; 1.
 DR PRINTS: PR00044; LEUZIPRMYC.
 DR SMART: SM00353; HLH; 1.
 DR PROSITE: PS00038; HLH; 1.
 DR PROSITE: PS00888; HLH-2; 1.
 KM Nuclear protein: DNA-binding; Proto-oncogene; phosphorylation.
 FT MOD_RES 212 219
 FT DOMAIN 212 242
 FT DOMAIN 220 242
 FT DNA_BIND 343 356
 FT DOMAIN 357 397
 FT DOMAIN 396 417
 FT MOD_RES 224 224
 FT MOD_RES 226 226
 FT MOD_RES 226 226
 SQ SEQUENCE 427 AA; 47140 MW; 6631FE6E615AE54B CRC64;
 Query Match 56.8%; Score 46; DB 1; Length 427;
 Best Local Similarity 61.5%; Pred. No. 25;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLQKGGPGGPP 13
 DB 144 EXLQKTPAPPP 156
 RESULT 9
 DYNL_CAEEL STANDARD; PRT; 830 AA.
 ID DYNL_CAEEL
 AC P39055; Q93176; Q950Y9;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dynamilin (EC 3.6.1.50).
 GN DYN-1 OR C02C6.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 OX [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RP STRAIN=Bristol N2;
 RX MEDLINE=97439883; PubMed=9294229;
 RA Clark S.G., Shurland D.L., Meyerowitz E.M., Bargmann C.I.,
 RA van der Bliek A.M.;

"A dynamin GTPase mutation causes a rapid and reversible temperature-inducible locomotion defect in *C. elegans*.";
Proc. Natl. Acad. Sci. U.S.A. 94:10438-10443(1997).
[2]
REVIEWS TO C-TERMINUS.
RA van der Bliek A.M.;
RN Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC STRAIN-Bristol N2;
RA Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
CC Submitter J.;
CC -1- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED IN PRODUCING MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN PARTICULAR ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: GTP + H₂O = GDP + phosphate.
CC -1- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; may be produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
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DR EMBL: L29031; AAB7228.2; -
DR EMBL: Z79596; CAB01857.1; -
DR EMBL: Z79596; CAC42251.1; -
DR WormPep: C02C6.1a; CE07833.
DR WormPep: C02C6.1b; CE07832.
DR HSP: O05193; 2DYN
DR InterPro: IPR001401; Dynamn.
DR InterPro: IPR000375; Dynamn_central.
DR InterPro: IPR001310; GED.
DR InterPro: IPR001849; PH.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00350; dynamn_1.
DR Pfam: PF01031; dynamn_2; 1.
DR Pfam: PF02212; GED; 1.
DR PRINTS: PR00195; DYNAMIN.
DR SMART: SM00053; DYN; 1.
DR SMART: SM00302; GED; 1.
DR SMART: SM00233; PH; 1.
DR PROSITE: PS00410; DYNAMIN; 1.
DR PROSITE: PS00003; PH_DOMAIN; 1.
KW Hydrolyase; Motor protein; GTP-binding; Microtubules; Multigene family;
KW Endocytosis; Alternative splicing.
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 138 142 GTP (BY SIMILARITY).
FT NP_BIND 207 210 GTP (BY SIMILARITY).
FT DOMAIN 519 624 PH.
FT VARSPLIC 817 830 PGSGPPNMAPPR -> VTPNSGAELIPARQVKKRP
(IN ISOFORM B).
FT CONFLICT 734 734 R -> P (IN REF. 1).
SQ SEQUENCE 830 AA: 93407 MW: FF681250E51AB8A5 CRC64;
Query Match 56.8%; Score 46; DB 1; Length 830;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID DPOD_MESAU STANDARD; PRT: 1103 AA.
AC P97283; P97284;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).
GN POLD1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Mishra N.C.;
RA Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: POSSIBLE TWO ENZYMAIC ACTIVITIES: DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOTIC ACTIVITY THAT DEGRADATES SINGLE STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED BY THE DNA POLYMERASE ALPHA/PRIME COMPLEX (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate + (DNA)(N).
CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 KDa, 50 KDa, 66 KDa and 12 KDa. The 125 KDa subunit contains the polymerase active site and most likely the active site for the 3'-5' EXONUCLEASE ACTIVITY (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES: ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS OF DNA SYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
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DR EMBL: U83704; AAB47254.1; -
DR EMBL: U83705; AAB47255.1; -
DR InterPro: IPR002064; DNA_POL_B.
DR InterPro: IPR004578; POL2.
DR Pfam: PF00136; DNA_POL_B; 1.
DR Pfam: PF03104; DNA_POL_B_exo; 1.
DR PRINTS: PR00106; DNAPOLB.
DR SMART: SM00486; POLB; 1.
DR TIGR: TIGR00592; pol2; 1.
DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein.
FT DOMAIN 4 19 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT ZN_FING 1008 1025 C4-TYPE (POTENTIAL).
FT ZN_FING 1054 1072 C4-TYPE (POTENTIAL).
FT VARIANT 64 64 MISSING (IN DELTA').
FT VARIANT 386 386 P -> S (IN DELTA').
SQ SEQUENCE 1103 AA: 123465 MW: 34AB5BF72DE53011 CRC64;
Query Match 56.8%; Score 46; DB 1; Length 1103;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

RESULT 10
DPOD_MOUSE

RESULT 11
DPOD_MOUSE

ID DPOD_MOUSE STANDARD: PRT: 1105 AA.
 AC P52431: 054883;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).
 GN POLDI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/c;
 RA MEDLINE=94085777; PubMed=8262377;
 RT Cullmann G., Hindges R., Borchert T.V., Hubscher U.;
 RT "Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of
 RT the homology boxes.";
 RL Gene 134:191-200(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Svj;
 RA Goldsby R.E., Singh M., Preston B.D.;
 RT "Mouse DNA polymerase delta gene (Pold1) maps to chromosome 7.";
 RL Mamm. Genome 9:92-93(1998).
 CC -1- FUNCTION: POSSESSES TWO ENZYMAIC ACTIVITIES: DNA SYNTHESIS
 CC (POLYMERASE) AND AN EXONUCLEOTYIC ACTIVITY THAT DEGRADATES SINGLE
 CC STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS
 CC ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND
 CC REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND
 CC SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED
 CC BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).
 CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa,
 CC 66 kDa and 12 kDa. The 125 kDa SUBUNIT CONTAINS THE POLYMERASE
 CC ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5'
 CC EXONUCLEASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC ALPHA, BETA, GAMMA, DELTA, AND Epsilon WHICH ARE RESPONSIBLE FOR
 CC DIFFERENT REACTIONS OF DNA SYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: Z21848; CAA79895.1;
 CC EMBL: AF024570; AAB99910.1;
 CC MGD: MG1:97741; Pold1.
 CC InterPro: IPR002064; DNA_POL_B.
 CC InterPro: IPR004578; Pold2.
 CC Pfam: PF00136; DNA_POL_B.1.
 CC Pfam: PF00104; DNA_POL_B-exo.1.
 CC PRINTS: PR00106; DNAPOLB.
 CC SMART: SMO0486; POLBc.1.
 CC TIGRFS: TIGR00592; pol2.1.
 CC TIGRFS: TIGR00592; pol2.1.
 CC PROSITE: PS00116; DNA_POLYMERASE_B.1.
 CC TRANSFAC: DNA-directed DNA polymerase; DNA replication;
 CC DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein.
 CC KW DNA-binding; Hydrolyase; NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 KM DOMAIN 4 19
 FT 2N-FING 1010 1027 C4-TYPE (POTENTIAL).
 FT 2N-FING 1056 1074 RPL -> GPP (IN REF. 2).
 FT CONFLICT 112 114 E -> K (IN REF. 2).
 FT CONFLICT 793 793 L -> F (IN REF. 2).
 FT CONFLICT 1000 1000 S -> Y (IN REF. 2).
 FT CONFLICT 1035 1035

FT CONFLICT 1045 1052 LEEFPRRL -> WKNSLRF (IN REF. 2).
 SQ SEQUENCE 1105 AA: 123783 MW: 53556C7620400564 CRC64;
 Query Match
 Best Local Similarity 56.8%; Score 46; DB 1; Length 1105;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 1 KRIQKGGGPPPK 14
 Db 4 KRQGGGPPPKR 17
 1 11 11 11 11
 RESULT 12
 ID GUNI_HOMIN STANDARD: PRT: 402 AA.
 AC P56680;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 GN CEL7B.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OC NCBI_TaxID=34413;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
 RX Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schuelein M.;
 RT "Oligosaccharide specificity of a family 7 endoglucanase: insertion
 RT of potential sugar-binding subsites.";
 RL J. Biochemol. 57:91-100(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE=98437137; PubMed=9761741;
 RA Mackenzie L.F., Sulzenbacher G., Dwyne C., Jones T.A., Woeldike H.F.,
 RA Schuelein M., Wilthers S.G., Davies G.J.;
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from
 RT Humicola insolens at 2.2 A resolution and identification of the
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
 RT intermediate.";
 RL Biochem. J. 335:409-416(1998).
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GUCCOSIDIC BONDS;
 CC (2) EXOCELLULOBIODOLASES THAT CUT THE DISACCHARIDE CELLULOSE
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 CC (3) BETA-1,4-GUCCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
 CC HYDROLASES).
 CC PDB: 1A39; 02-MAR-99.
 CC PDB: 2A39; 16-FEB-99.
 CC InterPro: IPR001722; GH_7.
 CC Pfam: PF00840; Glyco_hydro_7.1.
 CC ProDom: PD186135; GH_7.1.
 CC Cellulose degradation; Hydrolyase; Glycosidase; Glycoprotein;
 CC 3D-structure. 1 1
 KM MOD_RES 197 197 PYROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 202 202 NUCLEOPHILE.
 FT ACT_SITE 18 24 PROTON DONOR.
 FT DISULFID 51 73
 FT DISULFID 63 69
 FT DISULFID 140 365
 FT DISULFID 172 195
 FT DISULFID 176 194
 FT DISULFID 215 224
 FT DISULFID 223 228
 FT DISULFID 233 315

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .)
 SQ SEQUENCE 402 AA: 44577 MW: E0C0D31375D1635F CRC64:
 Query Match
 Best Local Similarity 47.4%; Score 45; DB 1; Length 402;
 Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
 OY 2 KLOGKGGG-----PPK 14
 DB 42 RAEGIGGCGCGDMGNPPK 60

RESULT 13
 FES_FSVST
 ID FES_FSVST STANDARD: PRT: 477 AA.
 AC P00543;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).
 GN V-FES.
 OS Feline sarcoma virus (strain Snyder-Theilen).
 OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.
 OX NCBI_Taxid=11780;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83050963; PubMed=6183005;
 RA Hampe A., Laprevotte I., Gallibert F., Fedele L.A., Sherr C.J.;
 RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
 RL evidence for a family of tyrosine-specific protein kinase genes.";
 CC Cell 30:775-785(1982).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC
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 CC modified and this statement is not removed. Usage by and for commercial
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02088; AAA3046.2; .
 DR PIR: A00652; TMVCS.
 DR HSP: P11362; IFGK.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 1
 DR Pfam: PF00069; Pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_Pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PolyProtein: Tyrosine-protein kinase; Oncogene; Transferase;
 KW ATP-binding; Phosphorylation; SH2 domain.
 FT DOMAIN 115 204
 FT NP_BIND 216 477
 FT BINDING 245 230
 FT BINDING 245 245
 FT ACT_SITE 338 338
 BY SIMILARITY.

FT MOD_RES 368 368 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 477 AA: 53756 MW: BB87EDBAE7A3BEB5 CRC64:
 Query Match
 Best Local Similarity 66.7%; Score 45; DB 1; Length 477;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 2 KLOGKGGGPPP 13
 DB 42 KLEQLGGEPPP 53

RESULT 14
 FES_FSVGA
 ID FES_FSVGA STANDARD: PRT: 609 AA.
 AC P00542;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).
 GN V-FES.
 OS Feline sarcoma virus (strain Gardner-Arnstein) (Ga-FesV) (Gardner-
 OC Arnstein feline leukemia oncovirus B).
 OX Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.
 OX NCBI_Taxid=11774;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83050963; PubMed=6183005;
 RA Hampe A., Laprevotte I., Gallibert F., Fedele L.A., Sherr C.J.;
 RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
 RL evidence for a family of tyrosine-specific protein kinase genes.";
 CC Cell 30:775-785(1982).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES
 CC POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02087; AAA3041.1; .
 DR PIR: A00651; TMVGC.
 DR HSP: P11362; IFGK.
 DR InterPro: IPR001060; Cdc15_Fes_GTP4.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_Pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00055; FCH; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00133; FCH; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_TYR; 1.
 DR PolyProtein: Tyrosine-protein kinase; Oncogene; Transferase;
 KW ATP-binding; Phosphorylation; SH2 domain.

FT DOMAIN 8 101 FCH.
 FT DOMAIN 247 336 SH2.
 FT DOMAIN 348 609 PROTEIN KINASE.
 FT NP_BIND 354 362 ATP (BY SIMILARITY).
 FT BINDING 377 377 ATP (BY SIMILARITY).
 FT ACT_SITE 470 470 BY SIMILARITY.
 FT MOD_RES 500 500 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 609 AA: 68769 MW: 5304919757CF73A3 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 609;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLOGKPGCGPP 13
 11: 111 111
 Db 174 KLEQLGCGEPP 185

RESULT 15
 FES_FELCA STANDARD: PRT: 820 AA.
 ID FES_FELCA
 AC P14238:
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
 FES OR FPS.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxId=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-8718954; PubMed-3553615;
 RA Roebroek A.J.M., Schalken J.A., Onnekink C., Bloemers H.P.J.,
 van de Ven W.J.M.;
 RA "Structure of the feline c-fes/fps proto-oncogene: genesis of a
 RT retroviral oncogene."
 RL J. Virol. 61:2009-2016(1987).
 CC -i CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -i SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
 CC SUBFAMILY.
 CC -i SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -i SIMILARITY: CONTAINS 1 FCH DOMAIN.
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 CC
 DR EMBL: M16705; AAA30808.1; -;
 DR EMBL: M16666; AAA30808.1; JOINED.
 DR EMBL: M16667; AAA30808.1; JOINED.
 DR EMBL: M16668; AAA30808.1; JOINED.
 DR EMBL: M16669; AAA30808.1; JOINED.
 DR EMBL: M16670; AAA30808.1; JOINED.
 DR EMBL: M16671; AAA30808.1; JOINED.
 DR EMBL: M16706; AAA30808.1; JOINED.
 DR EMBL: M16672; AAA30808.1; JOINED.
 DR EMBL: M16673; AAA30808.1; JOINED.
 DR EMBL: M16674; AAA30808.1; JOINED.
 DR EMBL: M16698; AAA30808.1; JOINED.
 DR EMBL: M16700; AAA30808.1; JOINED.
 DR EMBL: M16701; AAA30808.1; JOINED.
 DR EMBL: M16702; AAA30808.1; JOINED.
 DR EMBL: M16704; AAA30808.1; JOINED.
 DR PIR: A27824; TVCTFF.
 DR HSSP: P11362; IFCK.
 DR InterPro: IPR001060; Cdc15_Fes_CIP4.

DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00069; PKinase; 1.
 DR Pfam: PF00611; FCH; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Euk_pkinase; 1.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SM00055; FCH; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS0133; FCH; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR TRANSFERASE: T550001; SH2; 1.
 KW Phosphorylation; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 KW Phosphorylation; SH2 domain.
 FT DOMAIN 1 94 FCH.
 FT DOMAIN 458 547 SH2.
 FT DOMAIN 559 820 PROTEIN KINASE.
 FT NP_BIND 565 573 ATP (BY SIMILARITY).
 FT BINDING 588 588 ATP (BY SIMILARITY).
 FT ACT_SITE 681 681 BY SIMILARITY.
 FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 820 AA: 92974 MW: F3A52B750236834E CRC64;

Query Match 55.6%; Score 45; DB 1; Length 820;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KLOGKPGCGPP 13
 11: 111 111
 Db 385 KLEQLGCGEPP 396

Search completed: April 11, 2003, 16:11:52
 Job time : 2.98885 secs

COUNTRY: USA
ZIP: 21702-5012

COONING: 000
ZIP: 21702-5012


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FILE REFERENCE: VPI/98-14
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1584
TYPE: PRT
ORGANISM: DICDI - Dictyostelium Discoideum
US-09-457-040B-27

Query Match
Best Local Similarity 34.0%; Pred. No. 18; Length 1584;
Matches 16; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 16 APALANTIDVNDNNAGSGOOSVSNNEHNVANVNDNNGDSWNS 62
DB 436 SPSSINNEDISSNNNNNNNNNNNNNNNNNNNNNNNNNNNS 482

RESULT 6
US-09-187-124-2
Sequence 2, Application US/09187124A
Patent No. 625563
GENERAL INFORMATION:
APPLICANT: Emmertmann, Michael
APPLICANT: Kossmann, Jens
TITLE OF INVENTION: NOCLETIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
FILE REFERENCE: GFB8
CURRENT APPLICATION NUMBER: US/09/187,124A
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: PCT/EP97/02292
EARLIER FILING DATE: 1997-05-06
EARLIER APPLICATION NUMBER: DE 196 18 125.9
EARLIER FILING DATE: 1996-05-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 606
TYPE: PRT
ORGANISM: Solanum tuberosum
US-09-187-124-2

Query Match
Best Local Similarity 7.4%; Score 74; DB 4; Length 606;
Matches 14; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 40 VSVNNEHNVANVNDNNNGDSWNSIWDYGNCFATRLFOKK 79
DB 369 VTNNKHNLANGEDNKDGNHNSWNCGECEFASTFVKK 408

RESULT 7
US-09-463-238-5
Sequence 5, Application US/09463238
Patent No. 6469230
GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
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SEQ ID NO 5
LENGTH: 793
TYPE: PRT
ORGANISM: Solanum tuberosum
US-09-463-238-5

Query Match
Best Local Similarity 7.4%; Score 74; DB 4; Length 793;
Matches 14; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 40 VSVNNEHNVANVNDNNNGDSWNSIWDYGNCFATRLFOKK 79
DB 556 VTNNKHNLANGEDNKDGNHNSWNCGECEFASTFVKK 595

RESULT 8
US-09-463-238-14
Sequence 14, Application US/09463238
Patent No. 6469230
GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 838
TYPE: PRT
ORGANISM: Solanum tuberosum
FEATURE:
NAME/KEY: SITE
LOCATION: (274, 276)
OTHER INFORMATION: Xaa = unknown amino acid
US-09-463-238-14

Query Match
Best Local Similarity 7.4%; Score 74; DB 4; Length 838;
Matches 14; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 40 VSVNNEHNVANVNDNNNGDSWNSIWDYGNCFATRLFOKK 79
DB 601 VTNNKHNLANGEDNKDGNHNSWNCGECEFASTFVKK 640

RESULT 9
US-08-445-586-10
Sequence 10, Application US/08445586
Patent No. 5627050
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Ito, Toshimi
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Amami, Egon
TITLE OF INVENTION: Bone-related Sulfatase-Like protein and
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
```

ZIP: 20005-3314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/445,586

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/111,887

FILING DATE: 26-AUG-1993

APPLICATION NUMBER: JP 230030/92

FILING DATE: 28-AUG-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 324034/92

FILING DATE: 03-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Foreman, David S

REGISTRATION NUMBER: 33,694

REFERENCE/DOCKET NUMBER: 02481.1322-00000

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 533 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-445-586-10

Query Match

Best Local Similarity 7.4%; Score 73.5; DB 1; Length 533;

Matches 42; Conservative 20; Mismatches 48; Indels 47; Gaps 11;

QY 43 NNEHNVANDN-----NNGMD---SWNSTWD---YONGFAATRLFOKTCIYHKKKK 88
DB 291 NNTVFIFSDNGGOTLAGGNNPLGRKW-SLMEGVGVGVFVASPLKQGV-----KNR 345
QY 89 EVMPSIOSDALVK-----EKKLOG-----KGGCPPEPK-GLMSTVNPKNVDLSK 133
DB 346 ELIHSDMLPLVLKLRGHTNGTKRLODFDMKKITSESSPSRIELHNDIPNVDLS-SP 404
QY 134 FGKNIANMCRGIPYMAEMDEASLFTSGCTYTSV 170
DB 405 CPRN-----SNAPAKDSSLPEYS--AFNTSV 429

RESULT 10

US-09-134-001C-3235

Sequence 3235, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIORITY APPLICATION NUMBER: US 60/064,964

PRIORITY FILING DATE: 1997-11-08

PRIORITY APPLICATION NUMBER: US 60/055,779

PRIORITY FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3235

LENGTH: 467

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3235

Query Match 7.3%; Score 73; DB 4; Length 467;

Best Local Similarity 22.6%; Pred. No. 5.3;

Matches 21; Conservative 13; Mismatches 21; Indels 38; Gaps 2;

QY 5 IVEFALGVLAPLALAN-----IDVND 28
DB 308 ILIGATAIFGGMALNNNDKSDOKIANOSKRSKDKQAGSEDKKKSDSKNAD 367
QY 29 DNNAGSGQOSVSVNNEHNVANDNNGGWSN 61
DB 368 DSDMSSNPMTSTNNNDVAN--NNSNTYNN 398

RESULT 11

US-08-929-329-5

Sequence 5, Application US/08929329

Patent No. 6120770

GENERAL INFORMATION:

APPLICANT: Adams, John H

APPLICANT: Dalton, John P

APPLICANT: Kappe, Stefan

TITLE OF INVENTION: Plasmidum Proteins Useful for Preparing

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Barnes & Thornburg

CITY: Indianapolis

STATE: Indiana

COUNTRY: USA

ZIP: 46204

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929,329

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Breen, John P

REGISTRATION NUMBER: 38,833

REFERENCE/DOCKET NUMBER: 835910-28685

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 231-7745

TELEFAX: (317) 231-7433

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1507 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmidum yoe111

US-08-929-329-5

Query Match 7.3%; Score 73; DB 3; Length 1507;

Best Local Similarity 21.5%; Pred. No. 29;

Matches 46; Conservative 23; Mismatches 71; Indels 74; Gaps 12;

QY 19 LANYNDVND-----NNA-----GSGQOSVSVNNEHNV-----NDVNDGMD----- 58
DB 527 LKNTNDSSENSFTSHNTAPTHYEGNSKPSGTGNKRENTYCTOINLRNNNNYQPKN 586
QY 59 -----SWNSITMDYNGGFAATRLFOKTCIYHKKKKVEMPSIOGL 97
DB 587 KPNQAEYMDRFDIEKNHIIYIDMKQDGKTSG-----KL--KYNIISH-----ETADTIOGL 636
QY 98 -----DAIVKEKKLOGKGGGPPKGLMYSV--NPKNVDLSKFGKNIAMMG--IPTYM 149

DB 637 LITOKDICPNHYSBGRAGSCPNYKSIYVKTPESLNGNEHLSNPLNIRTYLKYM 696
QY 150 AEEM-----QEASLPFYSGTCTTSTWMTVIDISFC 179
DB 697 KSNVELPYEKSGLAMHGH-----DLISVC 719

RESULT 12

US-08-241-465B-19

; Sequence 19, Application US/08241465B

; Patent No. 5719125

; GENERAL INFORMATION:

; APPLICANT: FUJIO SUZUKI

; APPLICANT: YUJI HIRAKI

; APPLICANT: KAZUHIRO TAKAHASHI

; APPLICANT: JUNKO SUZUKI

; APPLICANT: JUN KONDO

; APPLICANT: ATSUKO KOHARA

; APPLICANT: AKIKO MORI

; APPLICANT: EI YAMADA

; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; COUNTRY: D.C.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: May 11, 1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-8850

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-241-465B-19

Query Match 7.2%; Score 72; DB 1; Length 334;

Best Local Similarity 19.0%; Pred. No. 4.3;

Matches 27; Conservative 27; Mismatches 76; Indels 12; Gaps 3;

QY 21 NYNIDVDDNNNAGSGQSVSVNNEHNVANVNNNGWDSMNSIMDYNGFAATRLFFQKKT 80
DB 76 HYTMSINGKLQDG-----SMEIDAGNNLETFKMGSGAEALAVNDPONGITGIRFAGGEK 130
QY 81 CIVHKMKKEVMPSTOSDALVYKKEKKLOGK-GPGGPPPKGLMYSVNPKNKYVDLSKFGKNIA 139
DB 131 CYTKAOKVKAIRPEVCAVTKOSISSKLEKIMPVKYEENSLIWAVDQPVKDNSSLSKVL 190
QY 140 NMCRGI-----PTYMAEEMOE 155
DB 191 ELGGDLPIFWLKPTYPEKIORE 212

RESULT 13

US-08-241-465B-20

; Sequence 20, Application US/08241465B

; Patent No. 5719125

; GENERAL INFORMATION:

; APPLICANT: FUJIO SUZUKI

; APPLICANT: YUJI HIRAKI

; APPLICANT: KAZUHIRO TAKAHASHI

; APPLICANT: JUNKO SUZUKI

; APPLICANT: JUN KONDO

; APPLICANT: ATSUKO KOHARA

; APPLICANT: AKIKO MORI

; APPLICANT: EI YAMADA

; TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; COUNTRY: D.C.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/241,465B

; FILING DATE: May 11, 1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-8850

; TELEFAX:

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 334 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-241-465B-20

Query Match 7.2%; Score 72; DB 1; Length 334;

Best Local Similarity 19.0%; Pred. No. 4.3;

Matches 27; Conservative 27; Mismatches 76; Indels 12; Gaps 3;

QY 21 NYNIDVDDNNNAGSGQSVSVNNEHNVANVNNNGWDSMNSIMDYNGFAATRLFFQKKT 80
DB 76 HYTMSINGKLQDG-----SMEIDAGNNLETFKMGSGAEALAVNDPONGITGIRFAGGEK 130
QY 81 CIVHKMKKEVMPSTOSDALVYKKEKKLOGK-GPGGPPPKGLMYSVNPKNKYVDLSKFGKNIA 139
DB 131 CYTKAOKVKAIRPEVCAVTKOSISSKLEKIMPVKYEENSLIWAVDQPVKDNSSLSKVL 190
QY 140 NMCRGI-----PTYMAEEMOE 155
DB 191 ELGGDLPIFWLKPTYPEKIORE 212

RESULT 14

US-08-227-108-16

; Sequence 16, Application US/08227108

; Patent No. 5807726

; GENERAL INFORMATION:

; APPLICANT: Blanchard, Claire

; APPLICANT: Benicourt, Claude

; APPLICANT: Junien, Jean-Louis

; TITLE OF INVENTION: Recombinant Dog Gastric Lipase

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Penile & Edmonds

; STREET: 1155 Avenue of the Americas

Page 6

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Crissey, Todd M.
/ REGISTRATION NUMBER: 37,807
/ REFERENCE/DOCKET NUMBER: 5072-DI-66-TWC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 734 622-7530
/ TELEFAX: 734 622-1553
/
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 380 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-073-674-16
/
Query Match 7 2%; Score 72; DB 2; Length 380;
Best Local Similarity 23.1%, Pred. No. 5.2;
Matches 39; Conservative 30; Mismatches 50; Indels 50; Gaps 11.
QY 22 YNIDVN---DDNNAGSGQGSVSVNNEHN-----VANVDNNN-----GWDSSW 60
| : : | | | : : | | | : : | | |
Db 38 YLEVNRIPIYGGKKNSGNTGQRPV-VFLQHGGLASATNMISNLPNNSLAFTIADAGYDVL 96
| : : | | | : : | | | : : | | |
QY 61 -NSIWDYNGCFATRLFPQKTCI-----VHKMKKEVNPSTIQSLDALVK--EKKLOGK 109
| : : | | | : : | : | : | : | : | : |
Db 97 GNS--RGNTWARRNLVYSPDSVEFMAFSPDEMAKYDLPA--TIDFIVKKTGQKQLHYV 151
| : : | | | : : | : | : | : | : | : |
QY 110 GPGGPPFKG-LMYSVNPKNVDLS-----KFGKNLIANMGKGI 146
| : : | | | : : | : | : | : | : | : |
Db 152 GHSQGTITGFIATFTNPSLAKRIKTFYALAPVATVYKTKSLINKLREVP 200
| : : | | | : : | : | : | : | : | : |

```


RESULT 9

A;Note: C0385C

NYL 297

A;Note: C0545C

Mismatches

77, gdp

259 N N E S I S N Y L N N Y K N N E S E N D I N G O T T H E

..cross-references: EMBL:X17488: NID:00053 <SC2>

1011 HNN 1079

... Bacillus subtilis


```

RA Koonin E.V., Shalloom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing Y., Aston C., Lai Z., Schwartz D.C., Perlea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL; AE001413; AAC71930.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 764 AA; 89327 MW; 0A80AF009269A3E CRC64;

Query Match          9.4%; Score 93; DB 5; Length 764;
Best Local Similarity 22.6%; Pred. No. 2.6;
Matches 31; Conservative 25; Mismatches 41; Indels 40; Gaps 6

QY      20 ANYNIDVNDNNAGSGOOSVSYNNEHVAVDNNNGWDSWNSIMDYGNGFAATRLFQKK 79
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      33S SNHNININHHNHSNNHNHNHNHNHNHNHNHNHNHNHNHNHNHNHYNYLYLTN-----YGR 386
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      80 TCIVHKMKKEVPISDIQLALYKELCKGCGRRPKGLMT-SVPRNKVD-----DL 131
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      387 ----HKNNTIPP-----PSGPPNNIKNVHPNNYNPPRPPPTL 424
       ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      132 SFEGKNIAMRCGIPIY 148
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      425 QTFNTN--DSFGKLSTY 439

RESULT 10

Q964F7 PRELIMINARY; PRT; 596 AA.
AC Q964F7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DF 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Merzoitze surface protein 8.
GN MSP8.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5633;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D10;
RX MEDLINE=21273140; PubMed=11378201;
RA Black C.G., Wu T., Wang L., Hibbs A.R., Coppel R.L.;
RT "Merozoite surface protein 8 of Plasmodium falciparum contains two
RT epidermal growth factor-like domains";
RL Mol. Biochem. Parasitol. 114:217-226(2001).
DR EMBL; AF325157; AAK63226.1; -.
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF_2.
SQ
SEQUENCE 596 AA; 69301 MW; 1F60185C4B01C5FD CRC64;

Query Match          9.2%; Score 91.5; DB 5; Length 596;
Best Local Similarity 33.9%; Pred. No. 2.7;
Matches 21; Conservative 15; Mismatches 15; Indels 11; Gaps 3;

QY      21 NYNIDVNDNNNAS-GGOOSVYNNEHVAVVDNNNGWDSWNSSIMDYNGGPA--ATRLFQ 77
       |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      59 NHNSNMNNNNNNNNDDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN-----MNGNGSFNPFKLF 110
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      78 KK 79
       ||
Db      111 KK 112

RESULT 11
Q964F5 PRELIMINARY; PRT; 600 AA.
```

DE Merozoite surface protein 8.
GN MSP8.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID:5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ITG2;
RX MEDLINE:21273140; PubMed=11378201;
RA Black C.G., Wu T., Wang L., Hibbs A.R., Coppel R.L.;
RT "Merozoite surface protein 8 of Plasmodium falciparum contains two
RT epidermal growth factor-like domains."; *J Biol Chem* 276:11421-11426(2001).
RL Mol. Biochem. Parasitol. 114:217-226(2001).
DR EMBL; AF325160; AAK63229.1; -;
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF; 2.
SQ SEQUENCE 600 AA; 69703 MW; 305371F642675034 CRC64;

[illegible]

RESULT 12			
ID	095NL3	PRELIMINARY:	PRT; 600 AA.
AC	095NL3:		
DT	01-DEC-2001 (TREMblrel, 19, Created)		
DT	01-DEC-2001 (TREMblrel, 19, last sequence update)		
DT	01-JUN-2002 (TREMblrel, 21, last annotation update)		
DE	Merozoite surface protein 8.		
GN	MSP8.		
OS	Plasmodium falciparum.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
OX	NCBI_TaxID=5833;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FVO, AND AA01:		
RX	MEDLINE=21273140; PubMed=11378201;		
RA	Black C.G., Wu T., Wang L., Hibbs A.R., Coppel R.L.;		
RT	"Merozoite surface protein 8 of Plasmodium falciparum contains two		
RL	epidermal growth factor-like domains.";		
RM	Mol. Biochem. Parasitol. 114:217-226(2001).		
DR	EMBL: AF325161; AAK63230.1; "-		
DR	EMBL: AF325159; AAK63228.1; "-		
DR	InterPro: IPR000561; EGF-like.		
DR	SMART: SM00181; EGF, 2		
SQ	SEQUENCE 600 AA: 69655 MW: A97870FFA9669FA CRC64:		

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Query Match          9.2%; Score 91.5; DB 5; Length 600;
Best Local Similarity 33.9%; Pred. No. 2.7;
Matches 21; Conservative 15; Mismatches 15; Indels 11; Gaps
QY 21 NYNTIDVDDNNNAAGS--GGQSVSYNNNEHHNVANNVNNNNCGMSDMSINDPYGNGFA--ATRLFO 77
      1 1 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 NHHNSMNNNNNNNNNNNDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
      59 NNGNGFSNFNFKKLGG 110
QY 78 KK 79
      1 1
Db 111 KK 112

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RESULT 13
Q8SSY0
ID Q8SSY0 PRELIMINARY; PRT; 628 AA

AC Q8SSY0: 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PMR-like protein, 10/100.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Eucelozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Elchingner L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tzungli B., Cox E., Quall M.A., Platzer M., Rosenthal A., Noegel A.A.,
RT Sequence and Analysis of Chromosome 2 of Dictyostelium.
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0115581; AAL92233.1; -
SQ SEQUENCE 628 AA: 72065 MW: 335F56D012173915 CRC64:

Query Match	9.2%	Score 91.5	DB 5	Length 628
Best Local Similarity	25.5%	Pred. No. 2.9		
Matches	36	Conservative	28	Mismatches 56; Indels 21; Gaps 5
QY	10	LLGVLAPALANTINIVDNDNNVAGSGQGSVSVNNEHVAVVNNNGMDNSNITWDGNG	69	
DB	230	LLGGLCEILISNSTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNK1-KTND	268	
QY	70	FAATRLFOKTCYVHKKKK--EYMPISLD-----ALVKE---KLGKGPQG	113	
DB	289	ISSDEQFOYEYELIINLTKPLNNMNSTFNVDLDSNLLATGLTIKNTFEIVRONSGW	348	
QY	114	PEPKGLMYSVNPKNVDLSKF	134	
DB	349	NSPAGLGXST---ARDISKF	365	

	RESULT	14
Q964F8		
ID	Q964F8	PRELIMINARY; PRT; 604 AA.
AC	Q964F8;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)	
DE	Merozoite surface protein 8.	
MSF8		
GN	Plasmodium falciparum.	
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
OX	NCBI_TaxID=5833;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRATN=NF7;	
RA	MEDLINE=21273140; PubMed=11378201;	
RX	Black C.G., Wu T., Wang L., Hibbs A.R., Coppel R.L.;	
RT	"Merozoite surface protein 8 of Plasmodium falciparum contains two	
RT	epidermal growth factor-like domains";	
RL	Mol. Biochem. Parasitol. 114:217-226(2001).	
DR	EMBL: AF325156; AAK63225.1; "	
DR	InterPro: IPR000561; EGF-like.	
DR	SMART: SM00181; EGF: 2.	
QO	SEQUENCE	604 AA; 70150 MW; E58CB8BEFC27DA66 CRC64;

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Query Match          9.1%; Score 90; DB 5; Length 604:
Best Local Similarity 31.4%; Pred.No. 3.8;      16; Indels 16; Gaps 3
Matches    22; Conservative 16; Mismatches
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Db 114 NFFNKLFGKK 123

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RESULT 15
ID 08SX72 PRELIMINARY; PRT; 868 AA.
AC 08SX72;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE LD30050p.
GN CG9381.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Change M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY094811; AAM1164.1;
SQ SEQUENCE 868 AA; 92619 MW; E6FF05B4392EE3B CRC64;

Query Match
Best Local Similarity 9.1%; Score 90; DB 5; Length 868;
Matches 31; Conservative 18; Mismatches 36; Indels 48; Gaps 5;

OY 23 NIDVN-----DDNNAGSGQSVSYNNEHNYANDNNNGWDSWNSITWDYGNCFATRLFO 77
Db 86 NVNLNGSGNSGNNNNNGN-----NNNNNGNISNNNNNNNNNN-----123
OY 78 KKTCTVHKMKKEVMPSTIOSLDALVKEKKLQGGKGGCGPEPKGLMYSVNPNKYVDLSEKFGKN 137
Db 124 -----KDNAPNCHS-----OGGPGCNSPDLGHNHQRGYNNGNNNRGLGNG 163
OY 138 IAN-MCRGIPPTM 149
Db 164 IVNGNTMGPPDYM 176

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 April 11, 2003, 16:06:33 : Search time 51.6281 seconds
 (without alignments)
 Run on: 474.899 Million cell updates/sec

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Perfect score:	993
Sequence:	1 MKLTMFVVGLGLLAPGFA.....TADILMLIRMSFCTSVET 184

Searched: 908470 seqs, 133250620 residues

Maximum DB seq logs	Match 0%
Post-processing:	Minimum Match 100%
Maximum Match	100%

Maximum Listing	Match first 45 summaries
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23: /SID52/gcgdata/geneSeq/geneSeqp_emb1/AA2003.DAT.*

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	936	94.3	184	23	AA008922	Human ORF γ protein
2	640	64.5	185	20	AAW93667	Human secreted pro
3	640	64.5	185	21	AAH24067	Human PRO1005 prot
4	640	64.5	185	21	AAH87272	Human signal pepti
5	640	64.5	185	21	AAV66686	Membrane-bound pro
6	640	64.5	185	22	AA865209	Human PRO1005 (pro
7	640	64.5	185	22	AA850357	Human PRO1005 prot
8	640	64.5	185	23	AA895452	Human angiotensin
9	640	64.5	185	23	AA884886	Human PRO1005 prot
10	640	64.5	185	23	AA083665	Human PRO protein

11	640	64.5	186	21	AAE383239
10	640	64.5	194	10	AAE69974
12	640	64.5	194	20	AAE76591
13	640	64.5	194	20	AAE33556
14	161	16.2	184	22	AAE04211
15	161	16.2	184	22	AAE04233
16	161	16.2	184	22	AAE64499
17	161	16.2	184	23	AAE64500
18	161	16.1	184	21	AAE68913
19	160	16.1	184	21	AAE65238
20	160	16.1	176	22	AAE29238
21	158.5	15.9	147	22	AAE04294
22	138.5	13.9	618	22	AAE63527
23	93	9.4	553	20	AAE55721
24	91	9.2	553	20	AAE53260
25	91	9.2	553	20	AAE41277
26	87	8.6	335	22	AAE99941
27	85.5	8.6	346	15	AAE55039
28	85.5	8.6	346	17	AAE91930
29	85.5	8.6	346	18	AAE35055
30	85.5	8.6	346	18	AAE19249
31	85.5	8.6	346	19	AAE43323
32	85.5	8.6	358	22	AAE38216
33	84.5	8.5	782	11	AAE06991
34	83.5	8.4	782	11	AAE82606
35	81.5	8.2	346	21	AAE18180
36	80.5	8.1	2295	21	AAE00897
37	80	8.1	95	22	AAE64069
38	80	8.1	2009	22	AAE71436
39	79.5	8.0	82	21	AAE54187
40	79.5	8.0	106	21	AAE75534
41	79.5	8.0	136	23	AAE63894
42	79.5	8.0	136	23	AAE65791
43	79.5	8.0	1215	21	AAE87284
44	79.5	8.0	1215	22	AAE81788
45	79	8.0	334	17	AAE00287

ALIGNMENTS

RESULT 1
ABP09922 1000 standard: Protein; 184 AA

XX
AC
ABP09922;

DT 24-JUN 2001
XX
sequence SEQ ID NO:19826

XX Human OREX protein sequence OREX;
DE
XX
XX Human: open reading frame; OREX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumour; hemorrhage;
KM hyperproliferative disorder; osteoarthritis; neurodegenerative disorder;
KM degenerative disorder; diabetes mellitus; systemic lupus erythematosus
KM cardiovascular disease; cholesterol ester storage disease;
KM hyperlipidosis; hypothyroidism; cholesteryl ester storage disease;
KM hyperlipidosis; hypothyroidism; cholesteryl ester storage disease;
KM immune deficiency; immune disorder; infectious disease;
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KM avastinemia gravis.

xx
05 Homo sapiens.

XX
PN
W0200192523-A2

XX
PD 06-DEC-2001.

2001WO-US10836

XX 30-MAY-2000; 2000US-206132P

PR 29-AUG-2007
XX

PA (cont.)

XX

Teach MD:

Shinkets KA, PI

Query Match	64.58;	Score 640;	DB 21;	Length 185;
Best Local Similarity	63.88;	Pred. No. 2.1e-60;		
Matches 118;	Conservative 34;			

	Indels	Gaps
1 MKLTFEVVGLGLLAPGEA-YTVNINGNDSNVDCGGCGGAGAA--	37	4
QY		3

```

1 MKETIVFAGLLGVLELAPALANYNINVN - DDNNAGSGGDSVSVMNNTETTS...
DB

```

WNSLMDYENSFAATRLFSKKSICIVHANKDAMPSLQDDLTMYKEOK--CKECCCAADKDT 22

118 MYSTICISM..... 119

120 MYSVNDPKVDVTGTHQWVLT
||||| :||| || |||||::|||
-----ALHACMGRLPTVAEEIPGNQLYSSKKCYTADILWLMSFC 177

178 GTSVE 182

b	180	GDIVE	184
---	-----	-------	-----

RESULT 5

AY66686 standard; protein: 100 %

AA166686;

05-APR-2000 (first entry)

membrane-bound protein PRO1005.

pharmaceutical; receptor immunoadhesin; LDL receptor; TIE ligand.

Homo sapiens.

MOJ303088-A2.

02-THU-1000

02-JUN-1998. 0000 0000-
-CNO 051425Z.

02-JUN-1998; 98US-0087609.
02-JUN-1998; 98US-0087750.

04-JUN-1998; 98US-0087827.
04-JUN-1998; 98US-0088021.

04-JUN-1998; 98US-0088025.
04-JUN-1998; 98US-0088028.

04-JUN-1998; 98US-0088030.
04-JUN-1998; 98US-0088030.
04-JUN-1998; 98US-0088030.

05-JUN-1998; 98US-0088326,
05-JUN-1998; 98US-0088167

05-JUN-1998; 98US-0088202.
05-JUN-1998; 98US-0088212.

09-JUN-1998; 9805-0088655.

1

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us-09-821-726a-16.rag

PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 04-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 12-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096765.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 17-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 18-AUG-1998; 98US-0097141.
 PR 19-AUG-1998; 98US-0097218.
 PR 20-AUG-1998; 98US-0097661.
 PR 24-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 PR XX (GETH) GENENTECH INC.
 PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WJ, Yuan J;
 PI XX
 DR N-PSDB: AA65023.
 DR WPI: 2000-072883/05.
 PT Membrane-bound proteins and related nucleotide sequences
 PS claim 12: Fig 139; 822pp: English.
 PS XX
 XX The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIR
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially

CC by recombinant techniques.

XX Sequence 185 AA;

SQ Query Match 64.5%; Score 640; DB 21; Length 185;

Best Local Similarity 63.8%; Pred. No. 2, 1e-60; Indels 4; Gaps 3;

Matches 118; Conservative 39; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKTTFVGLGLAAGPFA-YTVNINQDNCVDSQDSQDSVINGVYNNANIDNNNGWDS 59
 DB 1 MKTTFVGLGLAAGPFA-YTVNINQDNCVDSQDSQDSVINGVYNNANIDNNNGWDS 59
 OY 60 WNSLMDYENSPFATRLFSKSCIVHNNKNDAMPSLDIDITMYKQK--GKPGGAPPKDL 117
 DB 60 WNSLMDYENSPFATRLFSKSCIVHNNKNDAMPSLDIDITMYKQK--GKPGGAPPKDL 117
 OY 60 WNSLMDYENSPFATRLFSKSCIVHNNKNDAMPSLDIDITMYKQK--GKPGGAPPKDL 119
 DB 60 WNSLMDYENSPFATRLFSKSCIVHNNKNDAMPSLDIDITMYKQK--GKPGGAPPKDL 119
 OY 118 MYSVNPTRVEDLMTFPGKTAGMCRCITPYVAEPIGPPNOPLYSKKCYADILMLRMSFC 177
 DB 120 MYSVNPTRVEDLMTFPGKTAGMCRCITPYVAEPIGPPNOPLYSKKCYADILMLRMSFC 177
 OY 178 GTSVE 182
 DB 180 GTSVE 184

RESULT 6
 AAB65209 standard: Protein: 185 AA.
 ID AAB65209

AAB65209;

02-APR-2001 (first entry)

Human PRO1005 (UNC489) protein sequence SEQ ID NO:211.

Human: secreted and transmembrane protein; PRO: cytosolic;

cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

diagnostic assay.

Homo sapiens.

MO200073454-A1.

07-DEC-2000.

30-MAR-2000; 2000WO-US08439.

02-JUN-1999; 99WO-US12252.

23-JUN-1999; 99US-0141037.

07-JUL-1999; 99US-0143048.

20-JUL-1999; 99US-0144758.

26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222.

17-AUG-1999; 99US-0149396.

15-SEP-1999; 99WO-US21090.

08-OCT-1999; 99US-0158663.

01-DEC-1999; 99US-0158663.

16-DEC-1999; 99WO-US28301.

20-DEC-1999; 99WO-US30095.

05-JAN-2000; 2000WO-US00219.

11-FEB-2000; 2000WO-US03376.

18-FEB-2000; 2000WO-US04341.

22-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.

02-MAR-2000; 2000WO-US05841.

15-MAR-2000; 2000WO-US06884.

20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PS specific cells, to cause targeted cell death -
 Claim 12; Fig 139; 935pp; English.
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF4408 to AAF44269 and
 CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 SO Sequence 185 AA;

Query Match 64.5%; Score 640; DB 22; Length 185;
 Best Local Similarity 63.8%; Pred. No. 2.1e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVGLGLLAAPGFA-YTVNINGNDGVSINGVHVANINDNNNGDS 59
 Db 1 MKLTMEVGLGLLAAPGFA-YTVNINGNDGVSINGVHVANINDNNNGDS 59
 QY 60 WNSIMDYNGNGFAATRLRFOKTCIVHKMKKEVMPISIOIDLAVKEKKLOGKPGGPPKGL 119
 Db 60 WNSIMDYNGNGFAATRLRFOKTCIVHKMKKEVMPISIOIDLAVKEKKLOGKPGGPPKGL 119
 QY 118 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 Db 118 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 QY 120 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 Db 120 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 QY 178 GTSVE 182
 Db 178 GTSVE 182
 QY 180 GDIVE 184
 Db 180 GDIVE 184

RESULT 7
 AAB50957
 ID AAB50957 standard; Protein: 185 AA.
 XX AAB50957;
 AC AAB50957;
 DT 21-MAR-2001 (first entry)
 DE Human PRO1005 protein.
 DE Human PRO1005 protein.
 KW Human; PRO: cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 OS Homo sapiens.
 XX MO200073348-A2.
 XX PN 07-DEC-2000.
 PD 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US14941.
 PF 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US30999.
 PR 16-DEC-1999; 99WO-US30999.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 02-MAR-2000; 2000WO-US03441.
 PR 03-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000US-0187202.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 30-MAR-2000; 2000WO-US06884.
 PR 17-MAY-2000; 2000WO-US08439.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC,
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 DR WPI; 2001-016509/02.
 DR N-PSDB; AAC91559.

PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PS inflammatory, angiogenic and immunological disorders -
 PS Claim 31; Fig 14; 188pp; English.

CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, prostate cancer, ovarian cancer, colorectal
 CC cancer, uterine cancer, pancreatic cancer, renal cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukemia. They are also
 CC useful for treating other disorders such as neoplasia, glioma, astrocytoma,
 CC hypothalamic and other glandular, macrophage, epithelial, stromal and
 CC blastocoele disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 CC

SO Sequence 185 AA;

Query Match 64.5%; Score 640; DB 22; Length 185;
 Best Local Similarity 63.8%; Pred. No. 2.1e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVGLGLLAAPGFA-YTVNINGNDGVSINGVHVANINDNNNGDS 59
 Db 1 MKLTMEVGLGLLAAPGFA-YTVNINGNDGVSINGVHVANINDNNNGDS 59
 QY 60 WNSIMDYNGNGFAATRLRFOKTCIVHKMKKEVMPISIOIDLAVKEKKLOGKPGGPPKGL 119
 Db 60 WNSIMDYNGNGFAATRLRFOKTCIVHKMKKEVMPISIOIDLAVKEKKLOGKPGGPPKGL 119
 QY 118 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 Db 118 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 QY 120 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 Db 120 MYSVNPTRVEDLMTFGPKRIAGMCRGIPITYVAEELPGNQPUSKCYTADILMLTMSFC 177
 QY 178 GTSVE 182
 Db 178 GTSVE 182
 QY 180 GDIVE 184
 Db 180 GDIVE 184

XX 03-JAN-2002.
 PD 20-JUN-2001; 2001WO-US19692.
 XX 23-JUN-2000; 2000US-219637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000US-220664P.
 PR 02-AUG-2000; 2000WO-US20710.
 PR 17-AUG-2000; 2000US-222695P.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23522.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664510.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-070923P.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US30952.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 01-MAR-2001; 2001WO-US06520.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0808689.
 PR 10-MAY-2001; 2001US-0854208.
 PR 25-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 01-JUN-2001; 2001WO-US17443.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-090516/12.
 XX N-PSDB: ABL88141.
 DR One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 DR infarction), endothelial or angiogenic disorders in a mammal
 PS Claim 11; Fig 140; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC angiogenic, hypotensive, vascular and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC degeneration, atherosclerosis, hypertension, arterial stenosis,
 CC thrombocytopenia, angina, myocardial infarction, thrombocytopenia,
 CC lymphoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC probes used in the exemplification of the present invention.
 XX Sequence 185 AA:

Query Match
 Best Local Similarity 64.5%; Score 640; DB 23; Length 185;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;
 OY 1 MKLTFVVGILGLIAAGFA-YTVNINCGNDGVNDGSGQSVSINGVYINANINNNNGWS
 Db 1 MKFTVFAGLLGVFLAPALANNINVN-DINNNGSGQSVSINNEHANNVNNNGWS
 OY 60 WNSLMDYENSFAATRLFSKSCIVHRNKDAPSLDIDMVEOK--GKGGAAPPDL 117
 Db 60 WNSLMDYENGFAATRLFSKSCIVHRNKDAPSLDIDMVEOK--GKGGAAPPDL 117
 OY 118 MYSVNPTRVEDLNTGPRKIAICMGRIPTVYAEIPGPNDPLYSKCYADILMLIRMSFC 177
 Db 120 MYSVNPTRVEDLNTGPRKIAICMGRIPTVYAEIPGPNDPLYSKCYADILMLIRMSFC 177
 OY 178 GTSVE 182
 Db 180 GDIVE 184
 RESULT 10
 ID AAU83665
 AC AAU83665 standard; Protein: 185 AA.
 XX 08-MAY-2002 (first entry)
 DE Human PRO protein, Seq ID No 148.
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 OS Homo sapiens.
 XX WO200208288-A2.
 XX 31-JAN-2002.
 PD 29-JUN-2001; 2001WO-US21066.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 26-JUL-2000; 2000US-220666P.
 PR 28-JUL-2000; 2000US-220693P.
 PR 23-AUG-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23522.
 PR 15-SEP-2000; 2000WO-US23522.
 PR 10-NOV-2000; 2000US-000007P.
 PR 01-DEC-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 20-DEC-2000; 2000WO-US32678.
 PR 28-DEC-2000; 2000US-0747259.
 PR 10-MAY-2001; 2001WO-US34956.
 PR 25-MAY-2001; 2001US-0854280.
 PA (GETH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 XX N-PSDB: ABK33609.

CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AA08592-AA083713 represent human PRO
CC protein sequences of the invention

Query Match	64.5%	Score 640	DB 23	Length 185
Best local similarity	63.8%	Pred. No. 2	1e-60	
Matches 118	Conservative 24	Mismatches 39	Indels 4	Gaps 3

OY 1 MKLTMEVVGILGLLAAFGFA-YTVNINQNDGNAVDSGOOSYSINGVHNVANIDNNNGWDS 59
||| : |||| : | : : | : ||||||| : |||| : |||||||
Dd 1 MKRTIVFACILGVFLPALANYINVN-DDNNNAGSGQGSVSVNNEHNVANVDNNNGWDS 59

QY WNSLWDYENSFAATRLFSKSKSVIHKNNKDAMSLQDLIDINVEKK - GKGPGARPPKL 117
|||:||||| :|||::||| :|||:| ||||| |||
Db 60 WNSLDYDNGNFAATRLFOKKTCTIVHKNNKEVMSIQSLDALVYEKKLQGKGPPPKGL 119

```

QY      118 MYSVNRIVEDINTFGPKLAGMCRGIPITYVAELIPGNQPLYSKKCYADILWLIRMSFC 177
        ||||| :||: || |||||:|:|: : || ||| :||: |||
Db      120 MYSVNPKNVDLSKFGKNIANMCRGIPITYMAEENQEALEFPYSGTCYTTSVLMIYDISFC 179

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QY	178	GTSVE	182
		1 : 11	
Db	180	GDTVE	184

RESULT 11
AAB38329
ID AAB38329 standard; Protein: 186 AA.
vv

DT 31-JAN-2001 (first entry)
XX

Human secreted protein encoded by gene 9 clone HNSAD53.

KM immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KM cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
 KM neurotoxic; antibacterial; virucide; fungicide; ophthalmological;
 KM vulnery; gene therapy; infection; secreted protein.

OS Homo sapiens.

PN WO2000061623-A1

PD 19-OCT-2000.

06-APR-2000; 2000WO-US08979.

PR	09-APR-1999;	99US-0128693.
PR	26-APR-1999;	99US-0130991.

XX
PA (HUMA-) HUMAN GENOME SCI INC
XX

PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
PI Young PE;

DR WPI; 2000-647418/62

PT New nucleic acid molecules encoding 62 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -

PS Claim 11; Page 598; 716pp; English

CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
CC arrest; (d) cerebrovascular disorders e.g. cerebral ischaemia; (e)
CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
CC infections caused by bacteria, viruses and fungi; and (h) ocular
CC disorders e.g. corneal infection. The polypeptides can also be used to
CC aid wound healing and epithelial cell proliferation, to prevent skin
CC aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis.

SQ Sequence 186 AA.

Query Match	64.5%	Score 640;	DB 21;	Length 186;
Best Local Similarity	63.8%	Prod. No. 2.1e-60;		
Matches 118; Conservative	24;	Mismatches 39;	Indels 4;	Gaps 3

Dy
1 MKLTMFVGLLGLLAHPGFA-YTVNININGNDGNVDSSGGQSVSINCYNHVNANIDNNNGWDS 59

Dz
1 MKFTIYFAGLGVFLAPALANNINVN-DDNNNAGSGQGSVSNNNEHNVAVDNNGNWDS 59

QY 60 WNSLWDYENSFAATRLFEKSKSCIVHRRNNKKDAMPSLÖDLDTWVKEQ--GKGPGAAPPKDL 117
 |||:||||| |||||:|||||: |||: |||: ||||| |||
 Db 60 WNSLWDYNGNFAATRLFEQKCTCIVHKNNKEVMPISQSLDALVKEKKLDQKGPGGPAPPKGL 119

QY 118 MYSVNPTRVEDINTFGPKLAGMCRGIPITYVAEEIPGNQPLYSKKCYADILWLRMSFC 177
 ||||| : ||| : | | | | | | | | : | | ||| : ||| : |||
 Db 120 MYSVNPKNKVDLDSKFGKNTANMCRGIPITYMAEENQEAASLEFYSGTCYTTSVLWIVDISFC 179

QY	178	GTSVE	182
		1 : 11	
Db	180	GDTVE	184

RESULT 12	
AAW69974	
ID	AAW69974 standard; Protein; 194 AA

AC AAW69974;

DT 16-NOV-1998 (first entry)

Cancer associated protein.

KW Cancer; PCR; Northern blotting; ribonuclease protection assay;

XX	Synthetic
OS	

PN WO9837187-A1

27-AUG-1998.
 XX 18-FEB-1998; 98WO-JP00667.
 PF 21-FEB-1997; 97JP-0052508.
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 XX WPI; 1998-467552/40.
 DR
 XX
 PT Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 PS
 XX Claim 14; Page 64-65; 92pp; Japanese.
 XX
 CC The cancer associated proteins AAM6974-W6976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stingly hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 CC
 SQ Sequence 194 AA;
 Query Match 64.5%; Score 640; DB 19; Length 194;
 Best Local Similarity 63.8%; Pred. No. 2.2e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;
 QY 1 MKLTMEVGLLGLAARGFA-YTVNINNGNDGNGSQGSVSINGVHNVANINDNNNGMS 59
 DB 10 MKFTTFAGLGLVFLPALANININVA-DNNNAGSGQGSVSNNENHNAVANNNGMS 68
 QY 60 WNSLWDYENSFAATRLFSKSCIVHRMKNKAMPDLSLDLTMYEKQ--GKPGGAPPKDL 117
 DB 69 WNSIMDYGNGFPAATRLFKKTCIVHKMKKEVMPISLDAIVKEKKLOGKPGGPPKGL 128
 QY 118 MYSVNPTREVDLNTFGPKIAGMCRGIPITYAAEIPGPNOPLYSKKCTADILMLIRMSFC 177
 DB 129 MYSVNPNKVDLSKFGKNIANMCRGIPITYAAEIPGPNOPLYSKKCTADILMLIRMSFC 188
 QY 178 GTSVE 182
 DB 189 GDTVE 193
 RESULT 13
 AAY76591
 ID AAY76591 standard; Protein; 194 AA.
 XX
 AC AAY76591;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human ovarian tumor EST fragment encoded protein 87.
 XX
 KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX
 OS Homo sapiens.
 XX
 PN DE19817557-A1.
 XX
 PD 21-OCT-1999.

XX
 PF 09-APR-1998; 98DE-1017557.
 XX
 PR 09-APR-1998; 98DE-1017557.
 XX
 PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX WPI; 1999-591920/51.
 DR N-PSDB; AA277487.
 DR
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents
 PS
 XX Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (1) for
 CC recombinant expression of polypeptides (B) and (11) to isolate complete
 CC genes. (B) are used (1) to identify agents suitable for treatment of
 CC ovarian cancer; (11) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (111) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of the
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AA277450-277572.
 CC
 SQ Sequence 194 AA;
 Query Match 64.5%; Score 640; DB 20; Length 194;
 Best Local Similarity 63.8%; Pred. No. 2.2e-60;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;
 QY 1 MKLTMEVGLLGLAARGFA-YTVNINNGNDGNGSQGSVSINGVHNVANINDNNNGMS 59
 DB 10 MKFTTFAGLGLVFLPALANININVA-DNNNAGSGQGSVSNNENHNAVANNNGMS 68
 QY 60 WNSLWDYENSFAATRLFSKSCIVHRMKNKAMPDLSLDLTMYEKQ--GKPGGAPPKDL 117
 DB 69 WNSIMDYGNGFPAATRLFKKTCIVHKMKKEVMPISLDAIVKEKKLOGKPGGPPKGL 128
 QY 118 MYSVNPTREVDLNTFGPKIAGMCRGIPITYAAEIPGPNOPLYSKKCTADILMLIRMSFC 177
 DB 129 MYSVNPNKVDLSKFGKNIANMCRGIPITYAAEIPGPNOPLYSKKCTADILMLIRMSFC 188
 QY 178 GTSVE 182
 DB 189 GDTVE 193
 RESULT 14
 AAM23556
 ID AAM23556 standard; Protein; 184 AA.
 XX
 AC AAM23556;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST encoded protein SEQ ID NO: 1081.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.

XX Homo sapiens.
OS
XX WO200154477-A2.
PN
XX 02-AUG-2001.
PD
XX 25-JAN-2001; 2001WO-US02687.
PF
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werthman T;
XX
XX WPI: 2001-476164/51.
DR N-PSDB; AAH98215.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX Claim 20: Page 814-815; 1275pp; English.
PS
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 184 AA;
Query Match 16.2%; Score 161; DB 22; Length 184;
Best Local Similarity 26.6%; Pred. No. 5e-09;
Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;
OY 1 MKLIMFVGLGLLAAGFATV-NI---NGNDGVDGSGOOSVINCYNHVNANIDNNG 56
DB 1 MKLIVAEVLVTITGISHGVEFNITSPNNGNV---DETVIDNEKMAIINIAG 56
OY 57 WDSWNSLMDYENSPATRLFSKSCIVHRMKNKDAMPISLDDITWYKDEKKGPGAPPKD 116
DB 57 SCSTTTFEDKRGHGIASRVLSRACFLIKMDHONIPPLNNLQWYIEKQA-----LD 108
OY 117 LMS-----VNP--TRVEDLNTF--GPKIAGMCRGIPYVAEIPGPNOPLYSKKCYT 165
DB 109 NMFSSKYTWKYNPLESLIKVDWFLGSPLEKCKHPIPKGEVENTHN-VGAGCGCAK 167
OY 166 ADILWIRMSFC 177
DB 168 AGLIGLIGISIC 179
RESULT 15
AAE04211
ID AAE04211 standard; Protein: 184 AA.
AC AAE04211;
XX
XX 09-AUG-2001 (First entry)
DT
XX Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:66.
DE
XX
XX Human: secreted protein; proliferative disorder; cancer; tumour;
KW foetal abnormality; developmental abnormality; haematopoietic disorder;
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiotensin-related disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
KW endocrine disorder; infection; wound healing; vulvectomy;
KW cell culture; chemotaxis; food additive; chromosome 2;
KW binding partner identification.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label=signal_peptide
FT Protein 21..184
FT /note="Mature secreted protein"
XX
XX WO200136432-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-US31162.
XX
XX 19-NOV-1999; 99US-0166415.
XX 30-JUN-2000; 2000US-0215136.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Komatsoulis GA, Baker KP, Young PE;
PI WPI: 2001-343793/36.
XX N-PSDB; AAD08501.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Claim 11: Page 444; 509pp; English.
PS
XX AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
CC The secreted proteins and their genes are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 18 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiotensin disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin ageing due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein of the invention.
XX
SQ Sequence 184 AA;
Query Match 16.2%; Score 161; DB 22; Length 184;
Best Local Similarity 26.6%; Pred. No. 5e-09;
Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;

Mon Apr 14 14:01:47 2003

us-09-821-726a-16.rag

Page 12

[illegible]

Search completed: April 11, 2003, 16:11:12
Job time : 52.6281 secs

Mon Apr 14 14:01:50 2003

us-09-821-726a-16.ra1

Page 1

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 18.6101 Seconds
(without alignments)
290.907 Million cell updates/sec

Title: US-09-821-726A-16

Perfect score: 993
Sequence: 1 MKLIMFYVGLLGLAAGFA.....TADILWLRMSFGCTSVETRY 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2-6/p/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2-6/p/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2-6/p/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2-6/p/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2-6/p/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	9.2	553	US-09-083-351-2	Sequence 2, Appli
2	91	9.2	553	US-09-083-352-2	Sequence 2, Appli
3	85.5	8.6	346	US-08-213-403-2	Sequence 2, Appli
4	85.5	8.6	346	US-08-458-077-2	Sequence 2, Appli
5	85.5	8.6	346	US-08-460-741-2	Sequence 2, Appli
6	85.5	8.6	346	US-08-747-240-2	Sequence 2, Appli
7	85.5	8.6	346	US-08-299-567-6	Sequence 6, Appli
8	79.5	8.0	82	US-09-214-631-11	Sequence 11, Appli
9	79.5	8.0	336	US-08-436-044-2	Sequence 2, Appli
10	79	8.0	336	US-08-436-054-2	Sequence 2, Appli
11	79	8.0	336	PCT-US95-08812-2	Sequence 2, Appli
12	78	7.9	345	US-09-214-631-5	Sequence 5, Appli
13	77.5	7.8	428	US-09-118-319-5	Sequence 5, Appli
14	76	7.7	775	US-09-305-640-2	Sequence 2, Appli
15	75	7.6	334	US-08-241-465B-19	Sequence 19, Appli
16	75	7.6	334	US-08-241-465B-20	Sequence 20, Appli
17	73.5	7.4	521	US-09-071-035-64	Sequence 64, Appli
18	73.5	7.4	542	US-09-071-035-62	Sequence 62, Appli
19	73	7.4	238	US-09-216-295-12	Sequence 12, Appli
20	72	7.3	333	US-08-436-044-4	Sequence 4, Appli
21	72	7.3	333	US-08-436-054-4	Sequence 4, Appli
22	72	7.3	333	US-08-271-948-2	Sequence 2, Appli
23	72	7.3	333	US-08-271-948-2	Sequence 2, Appli
24	72	7.3	333	PCT-US95-08534-2	Sequence 4, Appli
25	72	7.3	333	PCT-US95-08534-2	Sequence 4, Appli
26	72	7.3	478	US-08-155-888-2	Sequence 2, Appli
27	71	7.2	193	US-08-616-368A-1	Sequence 1, Appli

28	71	7.2	193	4	US-09-054-298-1	Sequence 1, Appli
29	71	7.2	193	4	US-08-818-655-1	Sequence 1, Appli
30	70	7.0	193	1	US-08-616-368A-8	Sequence 8, Appli
31	70	7.0	193	1	US-08-616-368B-13	Sequence 13, Appli
32	70	7.0	193	2	US-08-739-485-1	Sequence 1, Appli
33	70	7.0	193	2	US-08-739-485-9	Sequence 8, Appli
34	70	7.0	193	4	US-09-054-298-8	Sequence 13, Appli
35	70	7.0	193	4	US-09-054-298-13	Sequence 8, Appli
36	70	7.0	193	4	US-08-818-655-8	Sequence 13, Appli
37	70	7.0	193	4	US-08-818-655-13	Sequence 4, Appli
38	70	7.0	312	1	US-08-525-505A-2	Sequence 2, Appli
39	70	7.0	312	1	US-08-525-505A-4	Sequence 1, Appli
40	70	7.0	992	1	US-08-127-499A-1	Sequence 1, Appli
41	70	7.0	992	1	US-08-482-847-1	Sequence 29, Appli
42	69.5	7.0	197	1	US-08-044-621D-29	Sequence 9, Appli
43	69.5	7.0	197	1	US-08-709-912-9	Sequence 9, Appli
44	69.5	7.0	197	2	US-09-047-370-9	Sequence 9, Appli
45	69.5	7.0	348	4	US-09-216-295-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-09-083-351-2
Sequence 2, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Palli, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HONG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.02
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-351-2
Query Match
Best local similarity 9.2%; Score 91; DB 3; Length 553;
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;
14 LAAGFAIYVINGNGNVDGSGQGSVINGVHNA-----NIDNNNGW----- 57

Db 76 MKKPPSYIALIT---MAIONAPDKKITLNGIOTIMDRPEPPYRNKOGMONSIRHNLSL 132
OY 58 -----DSWNSLMDYENS--FAATRLFSKSCSIYHRNNKDM 91
Db 133 NECFVVRPDDKKPGKGSYWTLPDPSYNN---FENGSLRRRRRRKKDKAYKDEKDR 189
OY 92 -----PSLQDLDTWKEOKGKGGAPPKDLMYSVPTREVEDINTGPRIAGMCRGIP 144
Db 190 HKEPPPGRRPPAPPEQADGNAPGPP-----PVRIDIKTEN---GTC----- 233
OY 145 TYVAEIEIGPNOPL 158
Db 234 -----PSPPOPL 240

RESULT 2

US-09-083-352-2
; Sequence 2, Application US/09083352
; Patent No. 6207450
; GENERAL INFORMATION:
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Darryl
; APPLICANT: Patil, Shiva
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,352
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-083-352-2

Query Match 9.2%; Score 91; DB 4; Length 553;
Best Local Similarity 19.6%; Pred. No. 0.1;
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;
OY 14 LAAPFATVYVINGNDGNDVDSGQSVSINGVHVA-----NIDNNNGW----- 57
Db 76 MKKPPSYIALIT---MAIONAPDKKITLNGIOTIMDRPEPPYRNKOGMONSIRHNLSL 132
OY 58 -----DSWNSLMDYENS--FAATRLFSKSCSIYHRNNKDM 91
Db 133 NECFVVRPDDKKPGKGSYWTLPDPSYNN---FENGSLRRRRRRKKDKAYKDEKDR 189
OY 92 -----PSLQDLDTWKEOKGKGGAPPKDLMYSVPTREVEDINTGPRIAGMCRGIP 144

Db 190 HKEPPPGRRPPAPPEQADGNAPGPP-----PVRIDIKTEN---GTC----- 233
OY 145 TYVAEIEIGPNOPL 158
Db 234 -----PSPPOPL 240

RESULT 3

US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-213-403-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;
Best Local Similarity 23.1%; Pred. No. 0.21;
Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;
OY 16 APGFATVYVINGNDGNDVDSGQSVSINGVHVAINDNNNG--WDSNNSLMDYENS--AAT 73
Db 195 APG-----SRGSLGDSGK-----HETVNOEESKSGRSGSGSDPDGPFNSKV 238
OY 74 RLFSK--KSCIV-----HRNNKDMPSLQDLDTWKEOKGKGGAP 113
Db 239 ALFAAVAGAGVIFLLITFLYVILKLRNRHRRKHQOAAALSTLASPKGSGSTAGTE 298
OY 114 PKDLMYSVPTREVEDINTGCP---KIAGMCRGIPTYVAEIEIGPNOPL---LTSK 161
Db 299 PSLLIPLTTE---NNCYPRYKVSQ--DYGHPYIYQENP--FOSPAITYRK 345

RESULT 4
US-08-458-077-2
; Sequence 2, Application US/08458077

Patent No. 5627267
 GENERAL INFORMATION:
 APPLICANT: Lyman, Stewart D.
 APPLICANT: Beckmann, M. Patricia
 APPLICANT: Baum, Peter R.
 APPLICANT: Carpenter, Melissa
 TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Apple System 7.1
 SOFTWARE: Microsoft Word for Apple, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,077
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/213,403
 FILING DATE: 15-MAR-1994
 APPLICATION NUMBER: US 07/977,693
 FILING DATE: 13-NOV-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2807-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 233-0644
 TELEFAX: (206) 587-0430
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-458-077-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;

QY 16 APGFAATVNINGNDGNDVSGGQOSVSTNGVHVANIDNNNG-WDSMNSLMDYENSF-AAT 73
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSQPGAGSGSDPDGFFNSKV 238

QY 74 RLFSK--KSCIV-----HRNKKDAMPISLQDLDTWKEOKGKPGGAP 113
 DB 239 ALFAAVGAGCVIFLLIIFLVLLKLRKRKHTQORAAALSLTLASPKGSGTAGTE 298

QY 114 PKDLMSVNPTRVEDLNTFGP---KIAGMCRGIPTYVAEELPGPNP--LYSK 161
 DB 299 PSDIILPLRTTE---NNYCPHYEKVSG-DYGHPIYIVQEMP--PQSPANIYYK 345

RESULT 5
 US-08-460-741-2
 Sequence 2, Application US/08460741
 Patent No. 5670625
 GENERAL INFORMATION:
 APPLICANT: Lyman, Stewart D.
 APPLICANT: Beckmann, M. Patricia
 APPLICANT: Baum, Peter R.
 APPLICANT: Carpenter, Melissa
 TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
 NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: Apple System 7.1
 SOFTWARE: Microsoft Word for Apple, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,741
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/213,403
 FILING DATE: 15-MAR-1994
 APPLICATION NUMBER: US 07/977,693
 FILING DATE: 13-NOV-1992
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2807-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-460-741-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;

QY 16 APGFAATVNINGNDGNDVSGGQOSVSTNGVHVANIDNNNG-WDSMNSLMDYENSF-AAT 73
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSQPGAGSGSDPDGFFNSKV 238

QY 74 RLFSK--KSCIV-----HRNKKDAMPISLQDLDTWKEOKGKPGGAP 113
 DB 239 ALFAAVGAGCVIFLLIIFLVLLKLRKRKHTQORAAALSLTLASPKGSGTAGTE 298

QY 114 PKDLMSVNPTRVEDLNTFGP---KIAGMCRGIPTYVAEELPGPNP--LYSK 161
 DB 299 PSDIILPLRTTE---NNYCPHYEKVSG-DYGHPIYIVQEMP--PQSPANIYYK 345

RESULT 6
 US-08-747-240-2
 Sequence 2, Application US/08747240
 Patent No. 5728813
 GENERAL INFORMATION:
 APPLICANT: Lyman, Stewart D.
 APPLICANT: Beckmann, M. Patricia
 APPLICANT: Baum, Peter R.
 APPLICANT: Carpenter, Melissa
 TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Apple System 7.1
 SOFTWARE: Microsoft Word for Apple, Version 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,240
 FILING DATE: 12-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/213,403
 FILING DATE: 15-MAR-1994
 APPLICATION NUMBER: US 07/977,693
 FILING DATE: 13-NOV-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Seese, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2807-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-747-240-2

Query Match 8.6%; Score 85.5; DB 1; Length 346;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;
 QY 16 APGFATVNINGNDGSGQSVSINGVHVNANINNNNG-WDSMNSLMDYNSF-AAT 73
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSGPGASGSSGDDPGFNSKV 238
 QY 74 RLFSEK--KSCIV-----HRNKDAMPSLDLDITVYKQKGGKPGAP 113
 DB 239 ALFAAVAGACVIFLLIIFLVLLKLRKRHRHTQORAAALSLSTLSPKSGSGTAGTE 298
 QY 114 PKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPTYVAEIPGPNP--LYSK 161
 DB 299 PSDIILPLRTTE---NNICPHYEKVSG-DYGHPIYIVQEMP-POSPANITYK 345

RESULT 7
 US-08-299-567-6
 Sequence 6, Application US/08299567
 Patent No. 5747033
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
 TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill River Road
 CITY: Tarrytown
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10591-6707
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,567
 FILING DATE: 01-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kempier, Gail M.

REGISTRATION NUMBER: 32,143
 REFERENCE/DOCKET NUMBER: REG 290
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-299-567-6

Query Match 8.6%; Score 85.5; DB 1; Length 346;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;
 QY 16 APGFATVNINGNDGSGQSVSINGVHVNANINNNNG-WDSMNSLMDYNSF-AAT 73
 DB 195 APG-----SRGSLGDSGK-----HETVNOEKSGPGASGSSGDDPGFNSKV 238
 QY 74 RLFSEK--KSCIV-----HRNKDAMPSLDLDITVYKQKGGKPGAP 113
 DB 239 ALFAAVAGACVIFLLIIFLVLLKLRKRHRHTQORAAALSLSTLSPKSGSGTAGTE 298
 QY 114 PKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPTYVAEIPGPNP--LYSK 161
 DB 299 PSDIILPLRTTE---NNICPHYEKVSG-DYGHPIYIVQEMP-POSPANITYK 345

RESULT 8
 US-09-214-631-11
 Sequence 11, Application US/09214631
 Patent No. 6413730
 GENERAL INFORMATION:
 APPLICANT: Holland, Sacha
 APPLICANT: Mbamalu, Geraldine
 APPLICANT: Pawsan, Tony
 TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
 TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
 FILE REFERENCE: 11757.23USMO
 CURRENT APPLICATION NUMBER: US/09/214,631
 EARLIER FILING DATE: 1999-03-12
 EARLIER APPLICATION NUMBER: PCT/CA97/00473
 EARLIER FILING DATE: 1997-07-04
 EARLIER APPLICATION NUMBER: 60/021,272
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 11
 LENGTH: 82
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-214-631-11

Query Match 8.0%; Score 79.5; DB 4; Length 82;
 Best Local Similarity 27.7%; Pred. No. 0.13;
 Matches 23; Conservative 14; Mismatches 35; Indels 11; Gaps 5;
 QY 84 HRNKDAMPSLDLDITVYKQKGGKPGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMC 140
 DB 5 HRKHTQORAAALSLSTLSPKSGSGTAGTEPSDIILPLRTTE---NNICPHYEKVSG-D 59
 QY 141 RGIPTVAEIPGPNP--LYSK 161
 DB 60 YGHPVYIVQEMP-POSPANITYK 81

RESULT 9
 US-08-436-044-2
 Sequence 2, Application US/08436044

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Patent No. 5624899
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,044
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90203
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-044-2

Query Match
Best local similarity 24.6%, Score 79; DB 1; Length 336;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9.
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,054
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 90201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-054-2

Query Match
Best local similarity 24.6%, Score 79; DB 2; Length 336;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9.
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[illegible]

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	Best Local Similarity	20.98;	Pred. No. 7.9;			
	Matches	31;	Conservative	18;	Mismatches	53; Indels 46; Gaps 5
QY	38 QSVSTNGVHYNAVANDNNNGDSWNSLMDVENF-----AATLEFSKSCSYIHRNKDA	90				
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Db	599 QSLNMGIGTILGHELTHTGYDDMGQIDBSGSLHMTWEASYSPELRKACIVRLAYDN--	656				
QY	91 MPTQLDLDITWVKCKGRKGAGAPPKDLMSVNPRTVEDLTFGKILGM-----CRGIP	144				
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Db	657 -----FTVYNQRVNQKHITLGENTADMGGLKLAHVAYO	688				
QY	145 TYVAEELPGPNOLYSKKCYTADILMIT	172				
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Db	689 KWRREH--GREPHLPRLK-YTHDOLFET	713				


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: Sequence 19, Application US/08241465B
: Patent No. 5719125
: GENERAL INFORMATION:
: APPLICANT: FUJIO SUZUKI
: APPLICANT: FUJI HIRAKI
: APPLICANT: KAZUHIRO TAKAHASHI
: APPLICANT: JUNKO SUZUKI
: APPLICANT: JUN KONDO
: APPLICANT: ATSUKO KOHARA
: APPLICANT: AKIKO MORI
: APPLICANT: EI YAMADA
: TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESS: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: COUNTRY: D.C.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/241,465B
: FILING DATE: May 11, 1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Warren M. Cheek, Jr.
: REGISTRATION NUMBER: 33,367
: REFERENCE/DOCKET NUMBER:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-8850
: TELEFAX:
: TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 334 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-241-465B-19

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Query Match 7.6%; Score 75; DB 1; Length 334;
Best Local Similarity 19.7%; Pred. No. 3.1;
Matches 29; Conservative 28; Mismatches 70; Indels 20; Gaps 4;

QY 21 YTVNINNG--NDGNVDGSGQGSVINGVHNVANIDNNNGDSWNSLMDYENSEFAATRLFSK 78
Db 77 YTMISNGKLDG-----SMETDAGNNLETFKMGSCAEFAIVNDFONGITGITRFAGG 128
QY 79 KSCIVHRNNKDPMSLDLDTMKVEQKGK---PGAPPKDLMSVNPTRVEDLNTFGPK 135
Db 129 EKCYIKAQVKARPEVGAFTKQSISSKLEKIMPVKYENSLIIVAVDQPVVDNSFLSK 188
QY 136 IAGMCRGIPTYVAEETPGNPOPLYSKK 162
Db 189 VLELCGLDPLTFWL-----KPTYPKE 208

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 Job time : 20.6101 secs

Mon Apr 14 14:01:53 2003

us-09-821-726a-16.rapb

Page 1

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 18.31 Seconds
(Without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726A-16

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Sequence: 1 MKLTMFVYGLGLIARFPA.....TADILWLRMSFGTSYERY 184

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published.Applications.AI.*
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2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	640	64.5	185	9	US-09-989-293A-211
3	640	64.5	185	9	US-09-989-735-211
4	640	64.5	185	9	US-09-990-444-211
5	640	64.5	185	9	US-10-001-054-14
6	640	64.5	185	9	US-09-989-730-211
7	640	64.5	185	9	US-09-990-436-211
8	640	64.5	185	9	US-09-991-181-211
9	640	64.5	185	9	US-09-993-687-211
10	640	64.5	185	9	US-09-989-734-211
11	640	64.5	185	9	US-09-997-653-211
12	640	64.5	185	9	US-09-993-667-211
13	640	64.5	185	9	US-09-990-438-211
14	640	64.5	185	9	US-09-990-562-211
15	640	64.5	185	9	US-09-997-428-211
16	640	64.5	185	9	US-09-997-666-211
17	640	64.5	185	9	US-10-227-884-148
18	640	64.5	185	9	US-09-990-711-211
19	640	64.5	185	9	US-10-230-163-148

20	640	64.5	185	9	US-09-989-726-211	Sequence 211, App
21	640	64.5	185	9	US-09-746-783-146	Sequence 146, App
22	640	64.5	185	9	US-09-980-437-211	Sequence 211, App
23	640	64.5	185	9	US-09-998-156-211	Sequence 148, App
24	640	64.5	185	9	US-10-218-631-148	Sequence 148, App
25	640	64.5	185	9	US-10-230-338-148	Sequence 211, App
26	640	64.5	185	9	US-09-991-157-211	Sequence 211, App
27	640	64.5	185	9	US-09-991-172-211	Sequence 211, App
28	640	64.5	185	9	US-09-997-514-211	Sequence 211, App
29	640	64.5	185	9	US-09-997-573-211	Sequence 211, App
30	640	64.5	185	9	US-10-050-704-105	Sequence 148, App
31	640	64.5	185	9	US-10-230-414-148	Sequence 211, App
32	640	64.5	185	9	US-09-990-443-211	Sequence 211, App
33	640	64.5	185	9	US-09-990-726-211	Sequence 211, App
34	640	64.5	185	9	US-09-997-559-211	Sequence 211, App
35	640	64.5	185	9	US-09-997-601-211	Sequence 211, App
36	640	64.5	185	9	US-09-989-729A-211	Sequence 211, App
37	640	64.5	185	9	US-09-990-440-211	Sequence 211, App
38	640	64.5	185	9	US-09-991-854-211	Sequence 211, App
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41	640	64.5	185	9	US-09-997-628-211	Sequence 211, App
42	640	64.5	185	9	US-09-997-683-211	Sequence 211, App
43	640	64.5	185	10	US-09-989-722-211	Sequence 211, App
44	640	64.5	185	10	US-09-989-723-211	Sequence 211, App
45	640	64.5	185	10	US-09-989-279-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-992-598-211
Sequence 211, Application US/09992598
Patient No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;
 Best Local Similarity 63.8%; Pred. No. 1,2e-59;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Caps 3;

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 DB 60 WNSLMDYENFATRLFSKSCVHRMNCAMPISLQDLTMYEKGK--GKGGGAPPKDL 117
 60 WNSIMDYGNEFATRLFOKKTCTVHKMKNEVMPSTQSLDALVKEKKLGKGGPPPKGL 119
 QY 118 MYSVNPTRVEDLNTFGPKIAGCMCRGIPITYAEIIPGNPLTKSKCYTADIIILMSFC 177
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 DB 178 GTSYE 182
 180 GDTVE 184

RESULT 2

US-09-989-293A-211

Sequence 211, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bolstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerder, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gueney, Austin L.

APPLICANT: Klijavio, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: US/09/989,293A

CURRENT FILING DATE: 2001-11-20

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PRIOR FILING DATE: 1997-06-16

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 118 MYSVNPTRVEDLMTFGPKRIAGMCRGIPTYVAEEIPGNOPLYSKCYTAIDITBRSFC 177
DB 120 MYSVNPTRVEDLMTFGPKRIAGMCRGIPTYVAEEIPGNOPLYSKCYTAIDITBRSFC 179
QY 178 GTSVE 182
DB 180 GDIVE 184

RESULT 3
US-09-989-735-211
Sequence 211, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61

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56	PRIOR APPLICATION NUMBER: 60/090535
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match 64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 MKLTFVYGLGLAAGFA-YTVNINGDNGVDSGQSVSINGVHNINNNNNWDS 59
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QY 60 WNSLMDVNSFAATRLFSKSCIVYHRNKDAPSLDDDMNEOK--GKPGGAPPKDI 117
DB 60 WNSLMDVNSFAATRLFSKSCIVYHRNKDAPSLDDDMNEOK--GKPGGAPPKDI 117
QY 118 MYSVNPVRVDLMTFGKTKAGMKRGIPYVAEIPGPNOPLYSKCKCYTADIMILMSFC 177
DB 120 MYSVNPVRVDLMTFGKTKAGMKRGIPYVAEIPGPNOPLYSKCKCYTADIMILMSFC 177
QY 178 GTSVE 182
DB 180 GDTVE 184

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RESULT 4
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Sequence 211, Application US/09990444
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 14
LENGTH: 185
TYPE: PRT
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US-10-001-054-14

Query Match 64.5% Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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60 WNSLMDVENSFAATRLCSKSCIVHRMKNKDMPSLQDIDTIVKBDK--GKGPGGAPPKL 119
Db 60 WNSLMDVENSFAATRLCSKSCIVHRMKNKDMPSLQDIDTIVKBDK--GKGPGGAPPKL 119
QY 118 MYSVPTREVDLNTFGPKIAGMCGEIPYVAEETPGNQPLYSKKCYTADILNLSFC 177
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QY 178 GTSVE 182
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Db 180 GDTVE 184

RESULT 6
US-09-989-730-211
Sequence 211, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavits, Iva J.
APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C69
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/09/989,730
PRIOR FILING DATE: 1997-06-16
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match Best Local Similarity 64.5%; Score 640; DB 9; Length 185;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 M K L M E V V G L I G L A P G F A - Y V N I N G N D G M V D S G Q S V S I N G V I N V A N I D N N N G M D S 59
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 DB 60 W N S I M D Y G N G F A A T R L O K K T C I V H K N K E M P S I O S L D A I V E K K I O G K P G G A P P K G L 119
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 QY 178 G T S V E 182
 DB 180 G D T V E 184

RESULT 7
 US-09-990-436-211
 Sequence 211, Application US/09990436
 Publication No. US20020198148A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerder, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
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APPLICANT: Gutney, Austin L.
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APPLICANT: Napier, Mary A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
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; PRIOR FILING DATE: 1998-07-09

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Query Match      64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.2e-55;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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DB 60 WNSIMWDGNFATRLFKOKTCTCYHKMKKEWDSIOSLDLALVEKKLDQGGPGGPPPKGL 119
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RESULT 8
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; Sequence 211, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Mon Apr 14 14:01:53 2003

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PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;
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DB 180 GDTVE 184

RESULT 9
US-09-933-687-211
Sequence 211, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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1	PRIOR APPLICATION NUMBER: 60/090355
2	PRIOR FILING DATE: 1998-06-23
3	PRIOR APPLICATION NUMBER: 60/090429
4	PRIOR FILING DATE: 1998-06-24
5	PRIOR APPLICATION NUMBER: 60/090431
6	PRIOR FILING DATE: 1998-06-24
7	PRIOR APPLICATION NUMBER: 60/090435
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9	PRIOR APPLICATION NUMBER: 60/090444
10	PRIOR FILING DATE: 1998-06-24
11	PRIOR APPLICATION NUMBER: 60/090445
12	PRIOR FILING DATE: 1998-06-24
13	PRIOR APPLICATION NUMBER: 60/090472
14	PRIOR FILING DATE: 1998-06-24
15	PRIOR APPLICATION NUMBER: 60/090535
16	PRIOR FILING DATE: 1998-06-24
17	PRIOR APPLICATION NUMBER: 60/090540
18	PRIOR FILING DATE: 1998-06-24
19	PRIOR APPLICATION NUMBER: 60/090542
20	PRIOR FILING DATE: 1998-06-24
21	PRIOR APPLICATION NUMBER: 60/090557
22	PRIOR FILING DATE: 1998-06-24
23	PRIOR APPLICATION NUMBER: 60/090676
24	PRIOR FILING DATE: 1998-06-25
25	PRIOR APPLICATION NUMBER: 60/090678
26	PRIOR FILING DATE: 1998-06-25
27	PRIOR APPLICATION NUMBER: 60/090690
28	PRIOR FILING DATE: 1998-06-25
29	PRIOR APPLICATION NUMBER: 60/090654
30	PRIOR FILING DATE: 1998-06-25
31	PRIOR APPLICATION NUMBER: 60/090655
32	PRIOR FILING DATE: 1998-06-25
33	PRIOR APPLICATION NUMBER: 60/090696
34	PRIOR FILING DATE: 1998-06-25
35	PRIOR APPLICATION NUMBER: 60/090862
36	PRIOR FILING DATE: 1998-06-26
37	PRIOR APPLICATION NUMBER: 60/090863
38	PRIOR FILING DATE: 1998-06-26
39	PRIOR APPLICATION NUMBER: 60/091360
40	PRIOR FILING DATE: 1998-07-01
41	PRIOR APPLICATION NUMBER: 60/091478
42	PRIOR FILING DATE: 1998-07-02
43	PRIOR APPLICATION NUMBER: 60/091544
44	PRIOR FILING DATE: 1998-07-01
45	PRIOR APPLICATION NUMBER: 60/091519
46	PRIOR FILING DATE: 1998-07-02
47	PRIOR APPLICATION NUMBER: 60/091626
48	PRIOR FILING DATE: 1998-07-02
49	PRIOR APPLICATION NUMBER: 60/091633
50	PRIOR FILING DATE: 1998-07-02
51	PRIOR APPLICATION NUMBER: 60/091978
52	PRIOR FILING DATE: 1998-07-07
53	PRIOR APPLICATION NUMBER: 60/091982
54	PRIOR FILING DATE: 1998-07-07
55	PRIOR APPLICATION NUMBER: 60/092182
56	PRIOR FILING DATE: 1998-07-09

Query Match	64.5%;	Score 640;	DB 9;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 1.2e-59;		
Matches 118: Conservation				

Local similarity 63.88; Pred. No. 1.2e-59;
Matches 118; Conservative 34.00; Zengchen 105;

indels 4; Gaps 3;

.....VGGDGLAHPGA-YTVINGNDGNVDGSGQSVSINGVHNVANIDNNGWDS 59
|||: ||||: | .|. .
||: |||: |

1 MKETIVEAGLGLVFLAPALANYINVN - DDNNAGSGGOOSVSVNNEFNVAITDWRGKST -

QY 60 WNSLWDYENSFAATRI.ESKKSCIVDNDWQZTUT 59

[illegible]

00 WNSIWIDYNGFAATRLFOKKTCTVHKMNKEVMPISQSLDALVKEKKLOGKGGPPKGT. 119

QY 118 MYSVNPTREVDLNTFGPKIAGMCRGIPTYVAEFTPGPNObi vcvrwrwa...

[illegible]

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QY 178 GTSVE 182
DB 180 GDIVE 184

RESULT 11
US-09-997-653-211
Sequence 211, Application US/09997653
Publication No. US20030080297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavio, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252

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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match 64.5%: Score 640; DB 9; Length 185;
 Best Local Similarity 63.8%: Pred. No. 1,2e-59;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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QY 1 KMLTMRVLLGLLAPGFA-YTVNINGDGNVDSGQSVSYNGVHNVANIDNNNGDWS 59
DB 1 MKFTTYFAGLTVFLAPALANINYN-DDNNAGSGQSVSYNHNANVNNNGDWS 59
QY 60 WNSLMDYENSPATRLFEKSCIVHRMKNDAFSLDDDTTWKECK--GKPGGAPPKDL 117
DB 60 WNSIMDYGNFPAIRLFQKCTIVHRMKNKEVPSIOSIDALVKEKKLGKGGGPPPKGL 119

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QY 118 MYSVNPTRVEDLNTFGKIGKCRGIPTYVAEIPGPNPLYSKCCYTADIIILMSFC 177
DB 120 MYSVNPKNKVDLSKFGKINAMCRGIPTVYAEEMQEAISLEFFSGTCTTSVLMIVDISFC 179
QY 178 GTSVE 182
DB 180 GDIVE 184

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RESULT 12
US-09-993-667-211
; Sequence 211, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; Acid Reference: F2730P1C4
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021

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Db 1 MKFTVAGLGLVFLAPALANYINYN-DDNNAGSGQGSVSNNEHNANVDNNNGWDS 59
 QY 60 MNSIMDYESPATRLRFKSKSCVHRMNDAMSLDDLTWKEQ--GKGPGADPKDL 117
 Db 60 MNSIMDYGCGFAATRLFKKCTVHRMNEVMSISSLALVKEKFKLOGKPGPPKGL 119
 QY 118 MYSVNPREDINTGPKTAGMCRGIPYVAEIRPPNPPLVSKKCYTADITLWLMSC 177
 Db 120 MYSVNPKNKDDLSKFGCKNIANNMCRGIPYMAEMQASLFFYSGCTYTSVLMIVDISFC 179
 QY 178 GTSVE 182
 Db 180 GDTVE 184

RESULT 13

US-09-990-438-211

Sequence 211, Application US/09990438

Publication No. US20030027734A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC3
 CURRENT APPLICATION NUMBER: US/09/990,438
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
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 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
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 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908

Mon Apr 14 14:01:53 2003

us-09-821-726a-16.rapb

Best Local Similarity 63.8%; Prod. No. 1.2e-59;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVGLIGLAPGFA-YTVNINCNDGNDVSGOOSTSINGVNVANINNNQWDS 59
Db 1 MKFTVFAGLIGVFLPALANYNVN--DDNNNGSGOOSTSVNNEHNVNNDNNQWDS 59
QY 60 WNSIMDYENSEFAATRLFSKSCIVHRMKNKDAMPISLQDIDTFVKKBOK--GKPGCAPPKDL 117
Db 60 WNSIMDYENSEFAATRLFSKSCIVHRMKNKDAMPISLQDIDTFVKKBOK--GKPGCAPPKDL 119
QY 118 MYSVNPTRVEDLMTFCPKIKGMRGIPYVAEIEGPNQPIYSKCKCYADILMLRMSFC 177
Db 120 MYSVNPTRVEDLMTFCPKIKGMRGIPYVAEIEGPNQPIYSKCKCYADILMLRMSFC 179
QY 178 GTSVE 182
Db 180 GDTVE 184

RESULT 14
US-09-990-562-211
Sequence 211, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Hong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C18
CURRENT APPLICATION NUMBER: US/09/990,562
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match

64.5%; Score 640; DB 9; Length 185;

1	PRIOR APPLICATION NUMBER: 60/089801
2	PRIOR FILING DATE: 1998-06-18
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4	PRIOR FILING DATE: 1998-06-18
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6	PRIOR FILING DATE: 1998-06-18
7	PRIOR APPLICATION NUMBER: 60/089947
8	PRIOR FILING DATE: 1998-06-19
9	PRIOR APPLICATION NUMBER: 60/089948
10	PRIOR FILING DATE: 1998-06-19
11	PRIOR APPLICATION NUMBER: 60/089952
12	PRIOR FILING DATE: 1998-06-19
13	PRIOR APPLICATION NUMBER: 60/090246
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65	PRIOR APPLICATION NUMBER: 60/091519
66	PRIOR FILING DATE: 1998-07-02
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69	PRIOR APPLICATION NUMBER: 60/091633
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72	PRIOR FILING DATE: 1998-07-07
73	PRIOR APPLICATION NUMBER: 60/091982


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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      64.5%; Score 640; DB 9; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,2e-59;
Matches 118: Conservative 24; Mismatches 39; Indels 4; Gaps 3;

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DB 1 MKETIVFAGLVFLPALANININ-DNNNAGSGOOSVNNHNANIDNNNGMDS 59
   11: 1111: 11 1111111: 1111: 1111111
QY 60 WNSLWDESFATRLSKSCIVHRMKNRAMPSTLDDLTWKEOK--GKGPGAPPKDL 117
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DB 60 WNSLWDESGFATRLFKKTCIVHRMKNRAMPSTLDDLTWKEOKGKGPGAPPKDL 119
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QY 118 MYSVNFRTVEDLTFGCPKLAGMCRGIPYVAEIPFPNPLVSKCYTIIILMFSFC 177
   1111111:1111: 11 1111111:1111: 11 1111 1111
DB 120 MYSVNFRTVEDLTFGCPKLAGMCRGIPYVAEIPFPNPLVSKCYTIIILMFSFC 179
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QY 178 GTSVE 182
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DB 180 GDTVE 184

RESULT 15
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; Sequence 211, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gettelson, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C44
; CURRENT APPLICATION NUMBER: US/09/997,428
; PRIOR FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 64.5%; Score 640; DB 9; Length 185;
 Best Local Similarity 63.8%; Pred. No. 1.2e-59;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVGLGLAPGA-YTVNINCDGNVDSGQSVSTNGVHNTANDNNNGWS 59
 DB 1 MKFTIVFAGILGVFLPALANTYNNV-DNNNAGSGQSVSTNNHNTANDNNNGWS 59
 QY 60 MNSIMDYENSEFATRLFSKSCIVHRANKDAMPISLODDTWKEDK--GKPGCAPPKDL 117
 DB 60 MNSIMDYGNFATRLFKKTCIVHRMKNKEVMPISLOSLDALVKEKKLGKPGCPPKGL 119
 QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPYVAEIPGPNQPLYSKKCYTADILMLMSFC 177
 DB 120 MYSVNPKNYDDLSKFGKNINAMNCRGIPYMAEMQEASLFFYSGTCTYTTVMIVDISPC 179
 QY 178 GTSVE 182
 DB 180 GDTVE 184

Search completed: April 11, 2003, 16:17:45
 Job time : 19.31 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 19.8108 Seconds
(without alignments)
892.885 Million cell updates/sec

Title: US-09-821-726a-16

Perfect score: 993
Sequence: 1 MKLTMFVYVGLGLLAAPGFA.....TADILMLRLMSFCGTSVETV 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	9.0	345	2	Stral/Epi92 protei
2	88.5	8.9	842	2	hypothetical prote
3	86.5	8.7	658	2	hypothetical threo
4	85.5	8.6	335	2	chondromodulin-1 p
5	85.5	8.6	346	2	elk ligand - human
6	85.5	8.6	539	2	phosphoenolpyruvat
7	85	8.6	345	2	phosphoenolpyruvat
8	84	8.5	643	2	hypothetical gene
9	83.5	8.4	782	2	lipoprotein associat
10	81	8.2	617	2	lipoprotein (impor
11	80.5	8.1	547	2	hypothetical prote
12	80.5	8.1	728	2	diacylglycerol kin
13	80.5	8.1	2295	2	probable membrane
14	80	8.1	3194	2	toxin-like outer m
15	79.5	8.0	539	2	phosphoenolpyruvat
16	79.5	8.0	1215	2	chitinase A (impor
17	79	8.0	186	2	hepatocellular prote
18	79	8.0	336	2	hepatocellular prote
19	79	8.0	138170	2	gene hrad protein
20	78	7.9	362	2	hypothetical prote
21	78	7.9	642	2	hypothetical prote
22	77.5	7.8	407	2	regulatory protein
23	77.5	7.8	419	2	hypothetical prote
24	77.5	7.8	459	2	hypothetical prote
25	77.5	7.8	1109	2	hypothetical prote
26	77.7	7.8	363	2	hypothetical prote
27	76.5	7.7	194	2	beta-cysteine-rich
28	76.5	7.7	493	1	cellulase (EC 3.2.
29	76.5	7.7	504	2	mucin (clone pgm31

30	76	7.7	631	2	T07670	probable protein k
31	76	7.7	1278	2	A71609	probable secreted
32	75.5	7.6	194	2	S41761	cysteine-rich prot
33	75.5	7.6	397	2	S64841	hypothetical prote
34	75.5	7.6	421	2	E64819	hypothetical prote
35	75.5	7.6	421	2	B90741	hypothetical prote
36	75.5	7.6	421	2	E85591	hypothetical prote
37	75	7.6	331	2	AG2679	conserved hypotet
38	75	7.6	352	2	E97461	hypothetical prote
39	75	7.6	423	2	T51794	MTB DNA-binding-11
40	74.5	7.5	404	2	S50648	hypothetical prote
41	74.5	7.5	624	2	B82108	flagellar hook-ass
42	74.5	7.5	747	2	S46608	TTA11 protein - ye
43	74.5	7.5	1045	2	S23570	pol polyprotein ho
44	74.5	7.5	1362	2	A75207	amylolipulanase P
45	74	7.5	241	2	S71473	endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1

148780 Stral/Epi92 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence.revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 148780; A55507; A55062; S52670
R:Bouillet, P.; Ould-Abdelghani, M.; Vitale, S.; Garnier, J.M.; Schubaur, B.; Doll
Dev. Biol. 170, 420-433, 1995
A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in p19 embryone
A:Reference number: 148780; MUID:9537533; PMID:7649373
A:Accession: 148780
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RFS>
A:Cross-references: EMBL:248781; NID:9747858; PIDN:CAA8695.1; PID:9747859
R:Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.
Genomics 24, 127-132, 1994
A:Title: Genomic organization and chromosomal localization of mouse Epi92, a gene enc
A:Reference number: A55507; MUID:95203867; PMID:7896266
A:Accession: A55507
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <RFS>
A:Cross-references: GB:U07598
R:Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A:Title: cDNA cloning and characterization of a ligand for the Cck5 receptor protein-
A:Reference number: A55062; MUID:95014510; PMID:7929389
A:Accession: A55062
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-89, 'T', 91-345 <SHA>
A:Cross-references: GB:U12963; NID:9575928; PIDN:AAA53231.1; PID:9575929
C:Genetics:
A:Gene: Epi92

Query Match 9.0%; Score 89; DB 2; Length 345;
Best Local Similarity 23.1%; Pred. No. 1.2;
Matches 40; Conservative 26; Mismatches 57; Indels 50; Gaps 10;

Oy	16	APGEVYTVINGNDGNVGS-----GQGSVSYNGVHNVANIDNNMGDSMSIMDYENSPFA 71
Db	195	APG-----RSGQSDSGKHETVQDEKSGGAGCGSGDSDSPFSKVAL-----FA 241
Oy	72	ATRLPFSKKSCTV-----HMMKNDAMPSSLODDLTVMKKEOKGKPGGAP 113
Db	242	AV-----GAGCVFLLIITFLVLLKLRHRRKHQOAAALSTLASPKGSGTAGTE 297
Oy	114	PKDLMSVNPPEVEDLNTFGP---KIAGMCRGIPYVAEEIPGNQP--LYSK 161
Db	298	PSDIIIPKYTE---NNICPKYEKVG--DIGHPIYIODEM-POSPANITYK 344

RESULT 2

T16198
hypothetical protein F28B4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Aug-2000
C:Accession: T16198
R:Leinbach, D.

submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F28B4.

A:Reference number: Z18475

A:Accession: T16198

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-842 <DEI>

A:Cross-references: EMBL:042834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4

C:Genetics:

A:Gene: CESP:F28B4.2

A:Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2

C:Superfamily: CDC25-type guanine nucleotide exchange activator homology

F:212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match

Best local Similarity 25.0%; Score 88.5; DB 2; Length 842;

Matches 27; Conservative 15; Mismatches 61; Indels 5; Gaps 2;

OY 29 DGNVDSGQGSVINGVHNVANIDNNNGWDSNLSMDYENSFAATRLFSKSCIVHNMK 88

DB 582 DGRLDGPPGPPVPLSGSTLPRGSNTNTPSSANASWTCGSEFPSSLPYS---HSRSK 637

OY 89 DAPPSLODDITMVKKQKGGKPGGAPKPDLMYSNPTRVEDLNTFGPKT 136

DB 638 GSESLQEVKTSM-STPRASADGTSQTSLRSATPIRTLAIEVDFSKV 684

RESULT 3

T41309

hypothetical threonine/asparagine-rich protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 08-Dec-2000

C:Accession: T41309; T40875

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wandbutt, R.; Wedler, E.

submitted to the EMBL Data Library, March 1998

A:Reference number: Z21986

A:Accession: T41309

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-658 <WOO1>

A:Cross-references: EMBL:AL022245; NID:94584240; PIDN:CAA18304.1; PID:g2995364; GSPDB:GN

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21954

A:Accession: T40875

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 468-658 <WOO2>

A:Cross-references: EMBL:AL031764; NID:93668147; PIDN:CAA21105.1; PID:g3668148; GSPDB:GN

A:Experimental source: strain 972h; cosmid c1235

C:Genetics:

A:Gene: SPDB:SPCC120.02c; SPDB:SPCC1235.01

A:Map position: 3

Query Match

Best local Similarity 8.7%; Score 86.5; DB 2; Length 658;

Matches 36; Conservative 26; Mismatches 53; Indels 27; Gaps 7;

OY 1 MKLTFVGLLGLAAPG-----ATTYVINGNDGSSGQGSVINGVHNV---ANI-- 51

DB 321 KETITIVVGNNSIPSONKSGKTFVSNANSSNS--DGSSSSLDVGSFVNAFKQIIVND 379

OY 52 ---DNNNGWDSNLSMDYENSFAAT-RLFSKRSCTIVHRNMKDPSPLODDITMVKKQK 107

DB 380 NSSNNSSGNTDSTIGYAAFAAAGKFFSOHSCDLASGNKSAQEGNQFLSWESE--- 436

OY 108 GPGGAPKPDLM-----YSVNPTR 125

DB 437 -----AKNLNMKNKYNISANQSO 452

RESULT 4

JT0569

chondromodulin-I precursor - bovine

N:Alternate names: 18K glycoprotein, cartilage; SCGP; small cartilage-derived glycopr

C:Species: Bos primigenius laurus (cattle)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999

C:Accession: JT0569; A33138; A36431

R:Hiiraki, Y.; Tanaka, H.; Inoue, H.; Kondo, J.; Kamizono, A.; Suzuki, F.

Biochem. Biophys. Res. Commun. 175, 971-977, 1991

A:Title: Molecular cloning of a new class of cartilage-specific matrix, chondromoduli

A:Reference number: JT0569; MUID:91222210; PMID:1709014

A:Accession: JT0569

A:Molecule type: mRNA

A:Residues: 1-335 <HIR>

A:Cross-references: GB:M65081; NID:g162840; PIDN:AAA30445.1; PID:g162841

A:Note: part of this sequence, including the amino end of the mature protein, was det

R:Name: P.J.; Treep, J.T.; Young, C.N.

submitted to the Protein Sequence Database, October 1990

A:Reference number: A33138

A:Accession: A33138

A:Molecule type: protein

A:Residues: 215-220, 'M', 222, 'N', 225-335 <NEA>

A:Note: 221-Val was also found

R:Name: P.J.; Treep, J.T.; Young, C.N.

J. Biol. Chem. 265, 9628-9633, 1990

A:Title: An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary st

A:Reference number: A36431; MUID:90277643; PMID:2351661

A:Accession: A36431

A:Molecule type: protein

A:Residues: 215-220, 'MNE', 224-225, 227-256, 'D', 257-335 <NE2>

A:Note: 221-Val was also found

A:Note: this sequence has been revised in reference A36535

R:Name: P.J.; Treep, J.T.; Young, C.N.

J. Biol. Chem. 265, 22056, 1990

A:Reference number: A36535

A:Contents: annotation; sequence revision

C:Comment: This protein stimulates DNA synthesis of cultured growth-plate chondrocyte

F:43-59/Domain: extracellular matrix; glycoprotein; transmembrane protein

F:215-335/Product: chondromodulin-I #status experimental <MAT>

F:223-236/Binding site: carbohydrate (Thr) (covalent) #status experimental

F:244/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:283-287, 284-324/Disulfide bonds: (or 283-324, 284-287) #status experimental

F:294-318, 298-314/Disulfide bonds: #status experimental

Query Match

Best local Similarity 8.6%; Score 85.5; DB 2; Length 335;

Matches 39; Conservative 29; Mismatches 70; Indels 37; Gaps 7;

OY 7 VVGLGLLAAPG-----ATTYVING--NDGNVDSGQGSVINGVHNVANIDN 53

DB 52 VLLLLAIGAFYPMKSGSDNIHYVHTWSINGKLQGS-----SMEIDAGNNLEFPK 103

OY 54 NNQWDSNLSMDYENSFAATRLFSKRSCTIVHRNMKDPSPLODDITMVK---EOKGK- 107

DB 104 GSGAEAVEYDFQNGITGRFAGGKCYIKAVKARIP---EVGMTKQSISSLEGGK 160

OY 108 GPGGAPKPDLMYSNPTRVEDLNTFGPKTAGMGRIPTYAAEILPBPNOPLYSKK 162

DB 161 MPVKYEENSLIIVAGQDPYKDNSFLSSKYLELGGDLPPIFWL-----KPTYPKE 208

RESULT 5

S46993

elk ligand - human

C:Species: Homo sapiens (man)

RESULT 11
T25478

Query Match 8.1% Score 80.5; DB 2; Length 728;
Post-Local Similarity 3.1%

Query Match 8.1%; Score 80.5; DB 2; Length 728;
 Best Local Similarity 24.1%; Pred. No. 19;
 Matches 34; Conservative 27; Mismatches 57; Gaps 7;

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 40.8222 Seconds
(without alignments)
928.727 Million cell updates/sec

Title: US-09-821-726A-16

Perfect score: 993
Sequence: 1 MKLMEVVGGLGLAAGFA.....TADILWLIRMSFGCTSVETV 184

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

SPTRMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_plant.*
10: sp_rodent.*
11: sp_virus.*
12: sp_vertebrate.*
13: sp_unclassified.*
14: sp_rv1r.*
15: sp_rv1r.*
16: sp_rv1r.*
17: sp_rv1r.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	23.6	191	11	09D0T7
2	167.5	16.9	184	11	09C0S6
3	93	9.4	618	5	09V6Z9
4	91	9.2	577	5	09V6Z9
5	89.5	9.0	292	5	025762
6	88.5	8.9	860	5	019852
7	88	8.9	2206	12	099FJ4
8	88	8.9	2206	12	099FJ4
9	86.5	8.7	658	3	059779
10	86	8.6	531	16	093JF5
11	85	8.7	2206	12	099FJ5
12	84	8.5	319	8	034834
13	83.5	8.4	782	5	090431
14	83.5	8.4	782	5	090431
15	83.5	8.4	782	5	090431
16	83.5	8.4	782	5	025730

17	83.5	8.4	782	5	026007	026007 plasmodium
18	83.5	8.4	3322	16	08X0Z5	08X0Z5 talsionia s
19	82.5	8.3	493	9	09JMB8	09JMB8 bacterioph
20	82	8.3	602	6	09GL34	09GL34 bos taurus
21	82	8.3	757	17	08T1V7	08T1V7 methanosarc
22	81	8.2	553	11	09QWR9	09QWR9 mus musculu
23	81	8.2	617	16	0980P1	0980P1 mycoplasma
24	80.5	8.1	547	5	P91006	P91006 caenorhabdi
25	80.5	8.1	782	5	025875	025875 plasmodium
26	80.5	8.1	1332	5	090430	090430 plasmodium
27	80.5	8.1	1782	5	098N17	098N17 drosophila
28	80.5	8.1	2295	5	09TY98	09TY98 plasmodium
29	80.5	8.1	868	5	08SX72	08SX72 drosophila
30	80	8.1	2009	5	09VXM0	09VXM0 drosophila
31	80	8.1	3194	16	09ZLM3	09ZLM3 helicobacte
32	79.5	8.0	494	2	005527	005527 comamonas a
33	79.5	8.0	1215	1	09UWR7	09UWR7 pyrococcus
34	79.5	8.0	1960	5	09UOK8	09UOK8 plasmodium
35	79.5	8.0	2432	12	0910P4	0910P4 aichi virus
36	79	8.0	186	5	001876	001876 caenorhabdi
37	79	8.0	338	4	015333	015333 homo sapien
38	78.5	7.9	501	5	09B1D4	09B1D4 anopheles g
39	78	7.9	319	3	096067	096067 neurospora
40	78	7.9	642	5	017169	017169 caenorhabdi
41	78	7.9	664	5	027435	027435 plasmodium
42	77.5	7.8	419	5	077316	077316 plasmodium
43	77.5	7.8	428	3	012646	012646 neocallima
44	77.5	7.8	439	3	092401	092401 agaricus bl
45	77.5	7.8	458	10	09FVH2	09FVH2 arabidopsis

ALIGNMENTS

RESULT 1

ID	PRELIMINARY:	PRT:	191 AA.
AC	09D0T7		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	1190003M12Rik protein.		
GN	1190003M12Rik.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=EMBRIO;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,		
RA	Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Williams L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,		
RA	Hayashizaki Y.		
RT	"Functional annotation of a full-length mouse cDNA collection."		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK004474; BAB23320.1;		
DR	MGI; 1916138; 1190003M12Rik.		

AC 01-NOV-1996 (TREMBlrel. 01, Created)
 AD 01-Oct-2001 (TREMBlrel. 18, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 GN Hypothetical 96.1 kDa protein.
 GN F28B4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderiinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None.
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Leinbach D.;
 RT "The sequence of C. elegans cosmid F28B4.";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: U42834; AAA83583.2; .
 DR HSP: Q61193; 1RLF.
 DR InterPro: IPR000651; RasGEFN.
 DR InterPro: IPR001895; RasGEF_CDC25.
 DR InterPro: IPR00159; RA_domain.
 DR Pfam: PF00786; RA_1.
 DR Pfam: PF00617; RasGEF; 1.
 DR Pfam: PF00618; RasGEFN; 1.
 DR SMART: SM00314; RA; 1.
 DR SMART: SM00147; RasGEF; 1.
 DR SMART: SM00229; RasGEFN; 1.
 DR PROSITE: PS00720; GDS_CDC25; 1.
 DR Hypothetical protein.
 KW SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;

Query Match 8.9%; Score 88.5; DB 5; Length 860;
 Best Local Similarity 25.0%; Pred. No. 7.6;
 Matches 27; Conservative 15; Mismatches 61; Indels 5; Gaps 2;

QY 29 DGNVDSGQGSVINGVHNVANINDNNNGWDSNLDYENSFAATRLFSKSKSCIVHMK 88
 DB 600 DGRDGGPPGPPVPLSGTSTPSSANTGSGSEFPSSLPFS---HSRSK 655
 QY 89 DAPSLDLDLTMYEKGKPGCAPPKDLMYSVNPTRVEDLNTFGPKT 136
 DB 656 SGESSLQEVKTSW-STRASADGTSGTSLRSATPLTRLAEEVDSKV 702

RESULT 7

QY 099FJ4 PRELIMINARY; PRT; 2206 AA.
 AC 099FJ4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 OS Polyprotein.
 OC Porcine teschovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OX NCBI_TaxID=118140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VIR 3764/86;
 RX MEDLINE-21105197; PubMed-11160660;
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
 RA Stelzner A., Prager D., Wurm R.;
 RT "Porcine teschoviruses comprise at least eleven distinct serotypes:
 RT Molecular and Evolutionary Aspects.";
 RL J. Virol. 75:1620-1631(2001).
 DR EMBL: AF296112; AAK12406.1; .
 DR HSP: Q88590; 1TMF.
 DR InterPro: IPR004004; CalliC_pol_hel.
 DR InterPro: IPR001676; RHV.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR Pfam: PF00073; Thv; 2.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00910; RNA_helicase; 1.
 DR PRINTS: PR00918; CALICVIRUSNS.
 SQ SEQUENCE 2206 AA; 247376 MW; 76FDA9AA1ADA08E CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;
 Best Local Similarity 24.1%; Pred. No. 27;
 Matches 52; Conservative 18; Mismatches 66; Indels 80; Gaps 11;

QY 4 TMFVGLGLIAPGAFAYVNING---NDGNVDSGQGSVINGVHNVANINDNNNGW- 58
 DB 275 TRHGGCLGVFAIPERSVFSKLOGIPLTYDGNKD-----ANSNI-----MDK 317
 QY 59 -----SNLSLMYENS-----FATRLFSKSKSCIVH-----RMN 87
 DB 318 FTTWHNPDMAMFGAWIYSHDITDKHWYKPKLEQYGGISPSOLF-----CFPHQLINPRTN 373

QY 88 KDAMPLODLD-----TMVEKQKGGPGCAPPKDLMYSVNPTRVEDLNT 131
 DB 374 SSATLCLEFVDCGPITDVTHCPMAIVVYVLRLETLVAGTSPSDINVSAPC---DVEY 430
 QY 132 FGPKIAGMCRG-IPTYVAEEIPGNQPLYSKSKCYTA 166
 DB 431 HGLRQDSMYGQPIPKF---DIDASKALFSTOPYTA 463

RESULT 8

QY 099FJ3 PRELIMINARY; PRT; 2206 AA.
 AC 099FJ3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 OS Polyprotein.
 OC Porcine teschovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OX NCBI_TaxID=118140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VIR 2500/99;
 RX MEDLINE-21105197; PubMed-11160660;
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
 RA Stelzner A., Prager D., Wurm R.;
 RT "Porcine teschoviruses comprise at least eleven distinct serotypes:
 RT Molecular and Evolutionary Aspects.";
 RL J. Virol. 75:1620-1631(2001).
 DR EMBL: AF296113; AAK12407.1; .
 DR HSP: Q88590; 1TMF.
 DR InterPro: IPR004004; CalliC_pol_hel.
 DR InterPro: IPR001676; RHV.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR Pfam: PF00073; Thv; 2.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00910; RNA_helicase; 1.
 DR PRINTS: PR00918; CALICVIRUSNS.
 SQ SEQUENCE 2206 AA; 247391 MW; 24C81E3E20C37405 CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;
 Best Local Similarity 24.1%; Pred. No. 27;
 Matches 52; Conservative 20; Mismatches 64; Indels 80; Gaps 12;

QY 4 TMFVGLGLIAPGAFAYVNING---NDGNVDSGQGSVINGVHNVANINDNNNGW- 58
 DB 275 TRHGGCLGVFAIPERSVFSKLOGIPLTYDGNKD-----ANSNI-----MDK 317
 QY 59 -----SNLSLMYENS-----FATRLFSKSKSCIVH-----RMN 87
 DB 318 FTTWHNPDMAMFGAWIYSHDITDKHWYKPKLEQYGGISPSOLF-----CFPHQLINPRTN 373
 QY 88 KDAMPLODLD-----TMVEKQKGGPGCAPPKDLMYSVNPTRVEDLNT 131
 DB 374 SSATLCLEFVDCGPITDVTHCPMAIVVYVLRLETLVAGTSPSDINVSAPC---DVEY 430
 QY 132 FGPKIAGMCRG-IPTYVAEEIPGNQPLYSKSKCYTA 166
 DB 431 HGLRQDSMYGQPIPKF---DIDASKALFSTOPYTA 463

RESULT 9

QY 059779 PRELIMINARY; PRT; 658 AA.
 AC 059779;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 OS Hypothetical 69.7 kDa ASN/THR-rich protein C320.02C in chromosome III.
 SC Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Medler H., Mambutt R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 468-658 FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL022245; CA18104.1;
 DR EMBL: AL031764; CA21105.1;
 KM Hypothetical protein.
 SO SEQUENCE 658 AA; 69695 MW; 63082230B6488AC5 CRC64;

Query Match 8.7%; Score 86.5; DB 3; Length 658;
 Best Local Similarity 25.4%; Pred. No. 8.5;
 Matches 36; Conservative 26; Mismatches 53; Indels 27; Gaps 7;

OY 1 MKLTFVGLGLLAPGF---AYTVNNGNDGNDGSGOQSVSYNGVHNV---ANI-- 51
 DB 321 METITIVGNNDSPSQNFKSGKTFVSNANSSNSN-DGSSSKSLDVGSFVNAFKQLNVND 379
 OY 52 ---DNNGWDSNLSMDYENSFAT-RLFSKKSCLVHRMNDAMPRLDDLTMYKEQKG 107
 DB 380 NSSNNSSGNDSTRTGAAVFAAGKFFESQHSCLASGKNSAOBGONFLSWESF--- 436
 OY 108 GPGGAPKCDL---YSVNPTR 125
 DB 437 -----AKNLAKTKTYSANQSO 452

RESULT 10
 O93JF5 PRELIMINARY; PRT; 531 AA.

ID O93JF5;
 AC 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Hypothetical protein StrAC16H6.07.
 GN StrAC16H6.07 OR SC05972 OR SCBAC16H6.07.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Collins M.R., Harris D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.M., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Jarke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL596162; CAC44586.1;
 DR InterPro: IPR000051; SAM_bind.
 KM Hypothetical protein.
 SO SEQUENCE 531 AA; 58656 MW; 714F103D5C29B3F CRC64;

Query Match 8.7%; Score 86; DB 16; Length 531;
 Best Local Similarity 28.4%; Pred. No. 7.3;
 Matches 27; Conservative 12; Mismatches 34; Indels 22; Gaps 4;

OY 96 DLDTWKEQKGGKGGAPKDLMSVNV--PFRVEDL-----NFGPKIAGCGRIPYV 147
 DB 92 DAVALVRGKGGKGGAPKDLMSVNV--PFRVEDL-----NFGPKIAGCGRIPYV 151
 OY 148 AEELP-----GPN--QPLYSKCYTAD 168
 DB 152 AESLPLRVERPALPARGGPDIVRLPEPLGWTVDV 186

RESULT 11
 O99FJ5 PRELIMINARY; PRT; 2206 AA.

ID O99FJ5;
 AC 099FJ5;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Polyprotein.
 OS Porcine teschovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Teschovirus.
 OX NCBI_TaxID=118140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VIR 918-19/85;
 RX MEDLINE=21105197; PubMed=11160660;
 RA Zell R., Dauber M., Krumbholz A., Henke A., Birch-Hirschfeld E.,
 RA Stelzner A., Prager D., Wurm R.;
 RT "Porcine teschovirus Compriase at Least Eleven Distinct Serotypes:
 Molecular and Evolutionary Aspects";
 RL J. Virol. 75:1620-1631(2001).
 RL EMBL: AF296111; AAK12405.1;
 DR HSP; Q88590; TMF.
 DR InterPro: IPR004004; Calic1_pol_hel.
 DR InterPro: IPR001676; RIV.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR Pfam: PF00073; rrv; 2.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00910; RNA_helicase; 1.
 DR PRINTS: PR00918; CALICVIRUSNS.
 SO SEQUENCE 2206 AA; 247295 MW; 113CC439CB2C774F CRC64;

Query Match 8.6%; Score 85; DB 12; Length 2206;
 Best Local Similarity 23.6%; Pred. No. 52;
 Matches 51; Conservative 21; Mismatches 64; Indels 80; Gaps 12;

OY 4 TMFVGLGLLAPGFAYTVNNG---NDGAVDGGGQSVSYNGVHNVANNDNNNGMD- 58
 DB 275 TRHGGCLGFAIFSVFSKLOGIPLTYDGNKG-----NVSNI-----MDR 317
 OY 59 --SMNS-----LMDYNSF-----AATRLFSKKSCLVH-----RMN 87
 DB 318 FTTHWHDAMFGAMYSATYDMDKDMYKPKLEQYGGISPSLFL---CFPHLLINPRN 373

QY 88 KDMPSLQDID-----TWMEQKGGKGGAPPKDLMYSVNPTRVEDLMT 131
 Db 374 SSATLCLPFVDCGPIFDVTVHCPMAIVVVYLRRLTVALGTSVDINVSAPC---DVEY 430
 QY 132 FGKINGMCRG-IPYVAEIEEPNPOLYKSKCYTA 166
 Db 431 HGLRQDSMYGPIPKF---DIDASKALFSSSTQPYTA 463

RESULT 12
 ID 034834 PRELIMINARY; PRT; 319 AA.
 AC 034834;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Intron orf.
 OS Kluveromyces lactis (Yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K8;
 RX MEDLINE=92035081; PubMed=1657415;
 RA Hardy C.M., Clark-Walker G.D.;
 RT "Nucleotide sequence of the COX1 gene in Kluveromyces lactis
 RT mitochondrial DNA: Evidence for recent horizontal transfer of a group
 RT II Intron."
 RL Curr. Genet. 20:99-114(1991).
 DR EMBL; X57546; CAA40768.1; -;
 DR InterPro; IPR004860; IAGLIDAGC_2.
 DR Pfam; PF03161; IAGLIDAGC_2; 1.
 KW Mitochondrion.
 SO SEQUENCE 319 AA; 37564 MW; 476288776D1P85 CRC64;

Query Match 8.5%; Score 84; DB 8; Length 319;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps 4;
 QY 24 NINGNDGNGVSGQGSVINGVHNVANIDNNNGDSMSLMDYEN---SFAATRLFSKKS 80
 Db 23 NHHNNNNNNPRGQSPFYGMTAGMKKINNNNSYNSYNNNNYNNKLTITGTNLYS--- 79
 QY 81 CIVHRNKKDAMPISLDLDTMYEOKGKGPGAPPKDLMYSVNPTRVED 128
 Db 80 ---NLNKKYNNNTM-IKYMIK-----IPNNIMMIGILLTD 113

RESULT 13
 ID 090431 PRELIMINARY; PRT; 782 AA.
 AC 090431;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Rhoptyr-associated protein 1 (Fragment).
 GN Rapi1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saul A.;
 RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins Rapi1 and
 RT Rapi2 of Plasmodium falciparum in Saimiri boliviensis monkeys."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF205282; AAF23403.1; -;
 FT NON_TER 782
 SO SEQUENCE 782 AA; 90066 MW; B344948D506F7DC CRC64;
 Query Match 8.4%; Score 83.5; DB 5; Length 782;

Best Local Similarity 24.0%; Pred. No. 20;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;
 QY 26 NGNDG-NDVSGGQGSVINGVHNVANIDNNNGDSMS---LMDYENFAATRLFSKKS 81
 Db 18 NVADGIVNGDNNYKGTI--INDFNFDYNYWPIPKKEFLNLYEDKFSSEFLKSS 75
 QY 82 IVHRNKKDAMPISLDLDTMYEOKGKGPGAPK-----DLMYSVNPTRV 126
 Db 76 V-----DDGNINLDTSTSNKSSK-KHGGRSVRSASAAALIEDDSKDDMEKASPSVY 129
 QY 127 EDLTFGPKTAGMCRGIPYVAEIEP 152
 Db 130 KTSTPGTQTSTGLKSSSPSSSTKSSP 155

RESULT 14
 ID 090429 PRELIMINARY; PRT; 782 AA.
 AC 090429;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Rhoptyr-associated protein 1.
 GN Rapi1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVO;
 RA Saul A.;
 RT "Efficacy of vaccines containing Rhoptyr-Associated Proteins Rapi1 and
 RT Rapi2 of Plasmodium falciparum in Saimiri boliviensis monkeys."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF205284; AAF23405.1; -;
 SO SEQUENCE 782 AA; 90041 MW; 27F2EA9BC930434E CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;
 Best Local Similarity 24.0%; Pred. No. 20;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;
 QY 26 NGNDG-NDVSGGQGSVINGVHNVANIDNNNGDSMS---LMDYENFAATRLFSKKS 81
 Db 18 NVADGIVNGDNNYKGTI--INDFNFDYNYWPIPKKEFLNLYEDKFSSEFLKSS 75
 QY 82 IVHRNKKDAMPISLDLDTMYEOKGKGPGAPK-----DLMYSVNPTRV 126
 Db 76 V-----DDGNINLDTSTSNKSSK-KHGGRSVRSASAAALIEDDSKDDMEKASPSVY 129
 QY 127 EDLTFGPKTAGMCRGIPYVAEIEP 152
 Db 130 KTSTPGTQTSTGLKSSSPSSSTKSSP 155

RESULT 15
 ID 090414 PRELIMINARY; PRT; 782 AA.
 AC 090414;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Rhoptyr associated protein-1.
 GN Rapi-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCCL/HN;
 RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF206631; AAF15365.1; -;

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 ; Search time 4.24796 Seconds
(without alignments)
290,907 Million cell updates/sec

Title: US-09-821-726A-13_COPY_78_119
Sequence: 1 KKTCLVHKMKRKPMSIOSL.....LVKKKIKGKGPGGPPKGL 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/laa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.5	26.9	269	US-07-857-224B-14	Sequence 14, Appl
2	59.5	26.9	269	US-07-857-224B-16	Sequence 16, Appl
3	57	25.8	467	US-09-002-361-3	Sequence 3, Appl
4	57	25.8	496	US-09-002-361-2	Sequence 2, Appl
5	53.5	24.2	494	US-09-126-420A-26	Sequence 26, Appl
6	53.5	24.2	542	US-08-701-380-2	Sequence 2, Appl
7	53.5	24.0	3174	US-09-032-365A-13	Sequence 13, Appl
8	53	24.0	199	US-08-477-451-3	Sequence 3, Appl
9	52	23.5	199	US-09-497-779A-6	Sequence 6, Appl
10	52	23.5	248	US-09-452-239-24	Sequence 24, Appl
11	52	23.5	248	US-09-452-239-26	Sequence 26, Appl
12	52	23.5	265	US-08-484-905-119	Sequence 119, App
13	52	23.5	265	US-08-481-985B-119	Sequence 119, App
14	52	23.5	265	US-08-370-476-119	Sequence 39, Appl
15	52	23.5	298	US-08-207-481-39	Sequence 41, Appl
16	52	23.5	331	PCT-US95-02689-41	Sequence 182, App
17	52	23.5	331	US-08-997-080-182	Sequence 182, App
18	52	23.5	331	US-08-997-362-182	Sequence 182, App
19	52	23.5	331	US-09-095-855-182	Sequence 182, App
20	52	23.5	331	US-09-324-542-182	Sequence 182, App
21	52	23.5	331	US-09-205-426-182	Sequence 182, App
22	51	23.1	247	US-09-452-239-18	Sequence 18, Appl
23	50.5	22.9	386	US-08-875-082-2	Sequence 2, Appl
24	50.5	22.9	752	US-09-817-180-2	Sequence 2, Appl
25	50.5	22.9	822	US-09-817-180-4	Sequence 4, Appl
26	50	22.6	428	US-08-332-576-2	Sequence 2, Appl
27	50	22.6	428	PCT-US95-13672-2	Sequence 2, Appl

28	50	22.6	673	US-09-078-347A-2	Sequence 2, Appl
29	49.5	22.4	469	US-08-363-215-1	Sequence 1, Appl
30	49.5	22.4	469	US-08-807-342B-6	Sequence 6, Appl
31	49	22.2	168	US-08-441-139-10	Sequence 10, Appl
32	49	22.2	280	US-09-383-586-18	Sequence 18, Appl
33	49	22.2	855	US-09-813-819-2	Sequence 2, Appl
34	49	22.2	855	US-09-920-048-2	Sequence 2, Appl
35	48.5	21.9	224	US-09-091-899-10	Sequence 10, Appl
36	48.5	21.9	376	US-08-874-569B-20	Sequence 20, Appl
37	48.5	21.9	1440	US-09-357-251-37	Sequence 37, Appl
38	48.5	21.9	1512	US-09-443-184-48	Sequence 48, Appl
39	48.5	21.9	3025	US-08-997-080-141	Sequence 141, App
40	48	21.7	73	US-08-997-362-141	Sequence 141, App
41	48	21.7	73	US-09-095-855-141	Sequence 141, App
42	48	21.7	73	US-09-324-542-141	Sequence 141, App
43	48	21.7	73	US-09-205-426-141	Sequence 141, App
44	48	21.7	73	US-09-562-737-70	Sequence 70, Appl
45	48	21.7	503		

ALIGNMENTS

RESULT 1
US-07-857-224B-14
Sequence 14, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESSES:
ADDRESS: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (international) 41 1 632 2830
TELEFAX: (international) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 269
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORGANISM: human
FEATURE: Protein kinase; Table 8 Column 15
PUBLICATION INFORMATION:
AUTHORS: Hanks, S. K.
AUTHORS: Hunter, T.
AUTHORS: Quinn, A. M.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-14

Query Match 26.9%; Score 59.5; DB 2; Length 269;
Best Local Similarity 39.4%; Pred. No. 3.1;
Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;
Qy 9 MKKEVMSIQLDALVKEK---LOGKGGPGPP 38
Db 34 LKKDVIQDDVDCTLVEKRVIALGGGPGGPP 66

RESULT 2

US-07-857-224B-16
; Sequence 16, Application US/07857224B
; Patent No. 5958784

GENERAL INFORMATION:

APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting folded structures of proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436

PRIOR APPLICATION DATA:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437

TELEX: none
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 269

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE:
DESCRIPTION: protein

ORGANISM: human
FEATURE: Protein kinase: Table 8 Column 17

PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988

US-07-857-224B-16

Query Match 26.9%; Score 59.5; DB 2; Length 269;
Best Local Similarity 39.4%; Pred. No. 3.1;
Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

Qy 9 MKKEVMSIQLDALVKEK---LOGKGGPGPP 38
Db 34 LKKDVIQDDVDCTLVEKRVIALGGGPGGPP 66

RESULT 3

US-09-002-361-3
; Sequence 3, Application US/09002361

Patent No. 6329516

GENERAL INFORMATION:

APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259

TELEX:
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

US-09-002-361-3

Query Match 25.8%; Score 57; DB 4; Length 467;
Best Local Similarity 36.8%; Pred. No. 12;
Matches 14; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

Qy 8 MKKEVMSIQLDALVKEKLOGKGGPG---PPPK 40
Db 314 QMKRQFTAVQKMA---EKKMQIDGPPGSAEPIPPPR 348

RESULT 4

US-09-002-361-2

; Sequence 2, Application US/09002361
; Patent No. 6329516

GENERAL INFORMATION:

APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-gated Chloride
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA

ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361

US-09-002-361-2
; Sequence 2, Application US/09002361
; Patent No. 6329516

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-002-361-2

Query Match 25.8%; Score 57; DB 4; Length 496;
Best Local Similarity 36.8%; Pred. No. 13;
Matches 14; Conservative 8; Mismatches 8; Indels 8; Gaps 2;
QY 8 KMKKEVPSIOSLALVKEKKLOGKPGG-----PPPK 40
Db 343 QMKRQFTAVQKMA---EKKMIDGPPSAPRIPPPR 377

RESULT 5
US-09-126-420A-26
Sequence 26, Application US/09126420A
Patent No. 6376753
GENERAL INFORMATION:
APPLICANT: BATTARD, YANNICK
APPLICANT: ROBINEAU, TIBURCE
APPLICANT: DURST, FRANCIS
APPLICANT: WERCK-REICHART, DANIELE
APPLICANT: DIDIERJEAN, LUC
TITLE OF INVENTION: PURIFIED CYTOCHROME P450 CYP76B1 FROM HELIANTHUS
TITLE OF INVENTION: TUBEROSUS AND ITS APPLICATIONS AS BIOCATALYST IN
TITLE OF INVENTION: PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL
TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S
FILE REFERENCE: 03715.0032
CURRENT APPLICATION NUMBER: US/09/126,420A
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: 60/054,351
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 494
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-126-420A-26

Query Match 24.2%; Score 53.5; DB 4; Length 494;
Best Local Similarity 40.6%; Pred. No. 38;
Matches 13; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

QY 13 VMPSTIOSLALV-----KEKKLOGKPGGPP 39
Db 8 LVASVAFSLVLMVSKORLISGLPPGPTP 39

RESULT 6
US-08-701-380-2
Sequence 2, Application US/08701380
Patent No. 5686598
GENERAL INFORMATION:

APPLICANT: NORTH, Michael
APPLICANT: NISHINA, Patsy
APPLICANT: NAGGERT, Juergen
TITLE OF INVENTION: GENES ASSOCIATED WITH RETINAL
TITLE OF INVENTION: DYSTROPHIES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,380
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-63565/PJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8700
TELEFAX: 415-494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-701-380-2

Query Match 24.2%; Score 53.5; DB 1; Length 542;
Best Local Similarity 35.4%; Pred. No. 42;
Matches 17; Conservative 7; Mismatches 15; Indels 9; Gaps 2;

QY 1 KKTCTYHKKMKKEVPSIOSLALVKEKKLOGKPGG-----PPPKGL 42
Db 135 KKEKILLPPKK--PLREKSSADLKERAKAGPRDGLSPPPPKPL 179

RESULT 7
US-09-032-365A-13
Sequence 13, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Naggert, Juergen
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF INVENTION: NEUROSENSORY DEFECTS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,365A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-032-365A-13

Query Match 24.2%; Score 53.5; DB 3; Length 542;
Best Local Similarity 35.4%; Pred. No. 42;
Matches 17; Conservative 7; Mismatches 15; Indels 9; Gaps 2;

OY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGG-----PPPKGL 42
Db 135 KKEKILPPKK---PLREKSSADLKERAKAGGPPGDLGSPDPKKPL 179

RESULT 8
US-08-477-451-3
Sequence 3, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
APPLICANT: Covaccl, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3174 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-3

Query Match 24.0%; Score 53; DB 2; Length 3174;

Best Local Similarity 42.3%; Pred. No. 3,6e+02;
Matches 11; Conservative 7; Mismatches 6; Indels 2; Gaps 1;
OY 6 VHKMKKEVMPSTQSLDALVKEKKLOG 31
Db 871 VHRLEKEQI--IOWLOTIIRNKKFQG 894

RESULT 9
US-09-497-779A-6
Sequence 6, Application US/09497779A
Patent No. 6297368
GENERAL INFORMATION:
APPLICANT: DEPINHO, RONALD A.
TITLE OF INVENTION: MYC HOMOLOG REGION II - ASSOCIATED PROTEIN AND USES THEREOF
FILE REFERENCE: 96700-609
CURRENT APPLICATION NUMBER: US/09/497,779A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 08/946,692
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 199
TYPE: PRT
ORGANISM: MOUSE
US-09-497-779A-6

Query Match 23.5%; Score 52; DB 4; Length 199;
Best Local Similarity 34.0%; Pred. No. 21;
Matches 16; Conservative 5; Mismatches 14; Indels 12; Gaps 2;

OY 8 KMKKEVMPSTQSLDALVKEK-----KLOG-KGPGGPPPKGL 42
Db 20 KKKSSPHLOKITKLTIVKSEDLAQSPLSKIRGPKAKGCPPKGL 66

RESULT 10
US-09-452-239-24
Sequence 24, Application US/09452239
Patent No. 6465229
GENERAL INFORMATION:
APPLICANT: Kataliski, Antoni J.
APPLICANT: Fader, Gary M.
TITLE OF INVENTION: Plant Gafeyo1-CoA O-methyltransferase
FILE REFERENCE: BB1284 US MA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 248
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: UNSURE
LOCATION: (7)
US-09-452-239-24

Query Match 23.5%; Score 52; DB 4; Length 248;
Best Local Similarity 32.3%; Pred. No. 27;
Matches 10; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOG 31
Db 126 EKAGVAHAKIDFREGPALPLDLVLIKDEKNGK 156

RESULT 11
US-09-452-239-26

Sequence 26, Application US/09452239
Patent No. 6465229
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni J.
APPLICANT: Fader, Gary M.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffey1-CoA O-Methyltransferase
FILE REFERENCE: B81284 US NA
CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 248
TYPE: PRT
ORGANISM: Glycine max
US-09-452-239-26

Query Match 23.5%; Score 52; DB 4; Length 248;
Best Local Similarity 32.3%; Pred. No. 27;
Matches 10; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCIVHKKKEVPSIOSDALVKKKLOG 31
DB 126 EKAGVAKHIDFREGPALPLDVLKDKKNG 156

RESULT 12
US-08-484-905-119
Sequence 119, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 119;

SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-119

Query Match 23.5%; Score 52; DB 2; Length 265;
Best Local Similarity 81.8%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 KPGGPPPKGL 42
DB 253 KPGGPPPKGL 263

RESULT 13
US-08-481-985B-119
Sequence 119, Application US/08481985B
Patent No. 601146

GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 119;
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-119

Query Match 23.5%; Score 52; DB 3; Length 265;
Best Local Similarity 81.8%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 KPGGPPPKGL 42
DB 253 KPGGPPPKGL 263

RESULT 14

US-08-370-476-119

Sequence 119, Application US/08370476

Patent No. 6153408

GENERAL INFORMATION:

APPLICANT: Mottiez, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Kourilsky, Philippe

APPLICANT: Lome, Yu-Chun

APPLICANT: Ojcius, David

APPLICANT: Castrouge, Armenda

TITLE OF INVENTION: Altered Major Histocompatibility Complex

NUMBER OF INVENTION: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370.476

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/117,575

FILING DATE: 07-SEP-1993

APPLICATION NUMBER: US 08/072,787

FILING DATE: 06-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05243.0001-01000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 119:

SEQUENCE CHARACTERISTICS:

LENGTH: 265 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-370-476-119

Query Match 23.5%; Score 52; DB 4; Length 265;
Best Local Similarity 81.8%; Pred. No. 29;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 KGPGRPPPKGL 42
||| |||| ||
Db 253 KGPGRPPPKGL 263

RESULT 15
US-08-207-481-39

Sequence 39, Application US/08207481

Patent No. 5820866

GENERAL INFORMATION:

APPLICANT: Kappler, John W.

APPLICANT: Marrack, Philippa
TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL
REGULATION
NUMBER OF INVENTION: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: SHERIDAN ROSS & MCINTOSH

STREET: 1700 LINCOLN STREET, SUITE 3500

CITY: DENVER

STATE: COLORADO

COUNTRY: USA

ZIP: 80202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/207,481

FILING DATE: 04-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kovarik, Joseph E.

REGISTRATION NUMBER: 33,005

REFERENCE/DOCKET NUMBER: 2879-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303/863-9700

TELEFAX: 303/863-0223

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 298 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-207-481-39

Query Match 23.5%; Score 52; DB 2; Length 298;
Best Local Similarity 81.8%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 KGPGRPPPKGL 42
||| |||| ||
Db 286 KGPGRPPPKGL 296

Search completed: April 11, 2003, 16:16:38
Job time: 5.24796 secs

Mon Apr 14 14:01:41 2003

us-09-821-726a-13_copy_78_119.rpr

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model
Run on: April 11, 2003, 16:07:53 ; Search time 4.52202 Seconds
(without alignments)
892.885 Million cell updates/sec

Title: US-09-821-726a-13_COPY_78_119
Perfect score: 221
Sequence: 1 KKTCTVHKMKKEVMPSTISL.....LVKEKKLQKGGPGPPPKGL 42

Scoring table: BL0SUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	64	29.0	1677	2	T14267	Xin protein, stage
2	61.5	27.8	311	2	H82966	probable transcrip
3	59.5	26.9	682	1	KIRBOG	protein kinase C (
4	59.5	26.9	697	1	KIRBOG	protein kinase C (
5	59.5	26.9	697	1	KIRBOG	protein kinase C (
6	59.5	26.9	697	2	JN0548	protein kinase C (
7	59.5	26.9	697	2	D2464	DNA topoisomerase
8	57.5	26.7	759	2	T24031	cell division prote
9	57.5	26.0	634	2	B70381	hypothetical prote
10	57.5	26.0	2459	2	H36812	period clock prote
11	57.5	25.8	997	2	S44457	NADH-ubiquinone ox
12	55.5	25.1	444	2	H82821	hypothetical prote
13	55.5	24.9	160	2	R89841	two-component resp
14	55.5	24.9	230	2	G83993	hypothetical prote
15	55.5	24.9	380	2	T29445	protein-tyrosine k
16	54.5	24.7	477	1	TVMCS	protein-tyrosine k
17	54.5	24.7	820	1	TVCPE	DNA topoisomerase
18	54.5	24.4	875	1	ITCAP	DNA gyrase subunit
19	54.5	24.4	875	1	B91018	DNA topoisomerase
20	54.5	24.4	891	2	AC0149	hypothetical prote
21	54.5	24.2	494	2	A71080	comparin 7-monoxy
22	53.5	24.2	502	2	T33030	probable regulator
23	53.5	24.0	233	1	H8RTAB	calteoyl-CoA O-met
24	53.5	24.0	233	1	T04084	class II histocomp
25	53.5	24.0	263	1	H8RTAB	dnak-type molecule
26	53.5	24.0	655	1	A37048	DNA gyrase, subunit
27	53.5	24.0	875	2	D85862	mRNA-binding prote
28	52.5	23.8	98	2	S15106	

30	52.5	23.8	156	2	S74733	hypothetical prote
31	52.5	23.8	303	1	S28392	protein-tyrosine-p
32	52.5	23.8	388	2	JC7510	benzoate X recepto
33	52.5	23.8	483	2	A97295	fusion of Uroporph
34	52.5	23.8	592	2	T29402	hypothetical prote
35	52.5	23.8	712	2	T12452	hypothetical prote
36	52.5	23.8	1189	2	S56852	hypothetical prote
37	52.5	23.5	148	2	T26759	major histocompat
38	52.5	23.5	233	2	I59495	H-2 class II histo
39	52.5	23.5	237	2	C60497	MHC class II histo
40	52.5	23.5	238	2	A53278	H-2 class II histo
41	52.5	23.5	252	1	HIMSBF	H-2 class II histo
42	52.5	23.5	263	1	HIMSBF	MHC class II histo
43	52.5	23.5	263	1	HIMSBF	MHC class II histo
44	52.5	23.5	263	1	HIMSBF	H-2 class II histo
45	52.5	23.5	263	2	A61389	MHC class II histo

ALIGNMENTS

RESULT 1
T14267
Xin protein, stage early embryo - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14267
R:Wang, D.Z., Lin, J.J.C.
submitted to the EMBL data library, March 1998
A:Description: Involved in a novel gene, Xin, in cardiac looping.
A:Reference number: 217948
A:Accession: T14267
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1677 <MAN>
A:Cross-references: EMBL:AF051945; NID:q2970645; PID:q2970646; PIDN:MAC06023.1
A:Experimental source: cardiac muscle; stage early embryo

Query Match 29.0%; Score 64; DB 2; Length 1677;
Best Local Similarity 30.6%; Pred. No. 17;
Matches 11; Conservative 10; Mismatches 3; Indels 12; Gaps 1;
QY 5 IVHKMKKEVMPSTISLALVKEKKLQKGGPGPPK 40
DB 561 MIHQEQD-----KPEEKGKGGPGPPK 584

RESULT 2
H82966
probable transcription regulator PA5437 [imported] - Pseudomonas aeruginosa (strain P
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H82966
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
..; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H82966
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <STO>
A:Cross-references: GB:AE004956; GB:AE004091; NID:9951760; PIDN:AA08822.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5437
C:Superfamily: transcription activator LysR-type
Query Match 27.8%; Score 61.5; DB 2; Length 311;
Best Local Similarity 37.5%; Pred. No. 5.8; Indels 7; Gaps 2;
Matches 15; Conservative 7; Mismatches 11

OY 4 C1VHMKREVPISQSLDLVKEK-----LOGK--GPGC 36
 Db 270 C1VHAKGKRLSPVAQAFVAFVEERKALISQLAGRPAGPGC 309

RESULT 3

KIRBOG
 protein kinase C (EC 2.7.1.1) gamma - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 R:Accession: C24664
 R:Consensus: L.; Parker, P.D.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fritschie, J.; 859-866, 1986
 A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity
 A:Reference number: A94291, MUID:86289426; PMID:3755548
 A:Accession: C24664
 A:Molecule type: mRNA
 A:Residues: 1-682 <OHN>
 A:Cross-references: GB:M13976; NID:9163525; PIDN:AAA30704.1; PID:9163526
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-stimulated phospholipid. This protein is a receptor for tumor-promoting phorbol ester, C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding F:3-13/Region: pseudophosphorylation motif
 F:6-11/Region: pseudophosphorylation motif
 F:86-135/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:136-249/Domain: protein kinase C C2 region homology <K22>
 F:334-599/Domain: protein kinase C C2 region homology <K23>
 F:342-350/Region: protein kinase ATP-binding motif
 F:21-51,54,70/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:34,37,59,62/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:86,116,119,135/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:98,102,124,127/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:365/Active site: Lys #status predicted
 F:653,640/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 682;
 Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

OY 9 MKKEVMPISQSLDLVKEK---LOGKPGPGP 38
 Db 367 LKKDVIQDDVDCTLVEKRVLALGGRPGGP 399

RESULT 4

KIRBOG
 protein kinase C (EC 2.7.1.1) gamma - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 R:Accession: A05105; S02129; I55317
 R:Koppl, J.L.; Lee, M.H.; Sultzman, L.A.; Kriz, R.W.; Loomis, C.R.; Hewick, R.M.; Bell, Cell 46, 491-502, 1986
 A:Title: Cloning and expression of multiple protein kinase C cDNAs.
 A:Reference number: A50883; MUID:86272097; PMID:3755379
 A:Accession: A05105
 A:Molecule type: mRNA
 A:Residues: 1-697 <KNO>
 A:Cross-references: GB:M13707; NID:9206186; PIDN:AAA1874.1; PID:9206187
 R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
 A:Title: Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat brain protein kinase C.
 A:Reference number: S02129; MUID:88262515; PMID:3387228
 A:Accession: S02129
 A:Molecule type: mRNA
 A:Residues: 1-697 <KNO>
 A:Cross-references: EMBL:X07287; NID:956917; PIDN:CAA30267.1; PID:956918
 R:Chen, K.
 J. Biol. Chem. 265, 19961-19965, 1990

A:Title: Characterization of the 5'-flanking region of the rat protein kinase C gamma
 A:Reference number: I55317; MUID:91060619; PMID:2246272
 A:Accession: I55317
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-56 <RSS>
 A:Cross-references: GB:M55417; NID:9206184; PIDN:AAA1873.1; PID:9554487
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-stimulated phospholipid. This protein is a receptor for tumor-promoting phorbol ester C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane C:Genetics: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 A:Genes: PRKC-gamma
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding F:18-28/Region: pseudophosphorylation motif
 F:21-26/Region: pseudophosphorylation motif
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:101-150/Domain: protein kinase C C2 region homology <K22>
 F:151-264/Domain: protein kinase C C2 region homology <K23>
 F:349-614/Domain: protein kinase C C2 region homology <K24>
 F:357-365/Region: protein kinase ATP-binding motif
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:48,52,74,77/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:101,131,134,150/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:114,117,139,142/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:380/Active site: Lys #status predicted
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 697;
 Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

OY 9 MKKEVMPISQSLDLVKEK---LOGKPGPGP 38
 Db 382 LKKDVIQDDVDCTLVEKRVLALGGRPGGP 414

RESULT 5

KIRBOG
 protein kinase C (EC 2.7.1.1) gamma - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 R:Accession: A28708
 R:Ohno, S.; Kawasaki, H.; Kono, Y.; Inagaki, M.; Hidaka, H.; Suzuki, K.
 Biochemistry 27, 2083-2087, 1988
 A:Title: A fourth type of rabbit protein kinase C.
 A:Reference number: A28708; MUID:88241036; PMID:2837282
 A:Accession: A28708
 A:Molecule type: mRNA
 A:Residues: 1-697 <OHN>
 A:Cross-references: GB:M19338; NID:9165651; PIDN:AAA3144.1; PID:9165652
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-stimulated phospholipid. This protein is a receptor for tumor-promoting phorbol ester C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding F:18-28/Region: pseudophosphorylation motif
 F:21-26/Region: pseudophosphorylation motif
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:101-150/Domain: protein kinase C C2 region homology <K22>
 F:151-264/Domain: protein kinase C C2 region homology <K23>
 F:349-614/Domain: protein kinase C C2 region homology <K24>
 F:357-365/Region: protein kinase ATP-binding motif
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:48,52,74,77/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:101,131,134,150/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:114,117,139,142/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:380/Active site: Lys #status predicted
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity 26.9%; Score 59.5; DB 1; Length 697;

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A:Reference number: A70300, MUID:98196666; PMID:9537320
A:Accession: B70381
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1,634 <AOF>
A:Cross-references: GB:AE000714, NID:92983446; PIDN:AA07029, 1
A:Experimental source: strain VF5
A:Genetics: fish

Query Match
Best Local Similarity 26.0%; Score 57.0
Matches
Keywords: cell division protein ftsH; ftsH/SEC18/CD48-type ATP-binding domain homology (P-loop)
169-379/Domain: ftsH/SEC18/CD48-type ATP-binding domain homology (P-loop)
195-202/Region: nucleotide-binding motif A (P-loop)

Qy	6	VHKMKKEVNPSTQSIDALVYEKKLQKRGSGPPRGL	42	Indels	5;	Gaps	1
Db	160	IEVEEVEKEIETLKDPVNFQTL-----GGRPKGV	191				
RESULT	10						

hypothetical protein ORF6 - gammaherpesvirus 1
C:Species: samaritaine herpesvirus 1
A:Note: host Samartine scuturus (CS)
Date: 16-Oct-1992 #sequence common squirrel monkey
Accession: H66812
H66812 Revision 16-Oct-1990

RESULT 10
#36812
#36812

NOV 191

A: Description: *Lamb* Data Library, January 1992
A: Reference number: Primary structure of the herpesvirus
A: Accession: H36806
A: Molecule: H36812
A: Residues: 1-2460
A: C: Residues: 1-2460
A: C: Residues: 1-2460

R:Altsch, J.C.; Lipman, D.J. *J. Mol. Biol.* 1990, 213, 405-432.
R:Altsch, J.C.; Lipman, D.J. *J. Mol. Biol.* 1990, 213, 405-432.
A:Title: Primary structure of the *Escherichia coli* 16S rRNA.
A:Reference number: A3709, 1990, the 16S rRNA gene.
A:Note: neither protein nor nucleotide sequence is given.
A:Genetic: 64
A:Gene: 64

Poetry Match	26.0%.	Score 57.5;	DB 2;
Best Local Similarity	41.0%;	Ptid. No. 1.6e+0;	Length 2469;
Matches 16;	Conservative 7;	Mismatches 9;	
Qy 5 IVHMKKFPPIOSLDLVAEKKKLGKKGPGP--			Indels 7; Gaps 2
Dd 1122 ILTKFVEEVLSEVKNL-----KEAKTKSLPLGNGPVFTDPK			1156
RESULT 11			

Period clock protein *fig - Sordaria fimicola*
 C:Species: *Sordaria fimicola*
 C:Date: 28-Oct-1994 #sequence
 C:Accession: S44457
 R:Merrow, M.W.; Dunlap, J.C.
 EMBL J. 13, 2257-2266, 1994
 A:Title: Intergenic complementation of a circadian rhythmicity defect: phylogenetic
 A:Reference number: S4457; MUID:94252311; PMID:8194516
 A:Accession: S4457
 A:Molecule type: DNA
 A:Residues: 1-997 <EMBL>
 A:Cross-references: EMBL:U4467; NID:9310366; PIDN:AAA20825.1; PTD:9530050
 C:Genetics:
 A:Gene: *fig*

C; Keywords: citizenship

Query Match

Best Local Similarity	25.88;	Score 57;	DB 2;	Length 997;
Matches 17; Conservative 10;	Mismatches			

Oy I KKTCTTTC.....

	Indels	14;	Gaps	3
Db	: ::::	EVMSPTQSD--ALVNEKKFLDGGCGGPPPG	41		
	320 KAKLVRLRDLFTGRISGNMORIPSPMDALVSEGTIN--APPRPPEG				
	HH82821				
RESULT	12				

Name: NADH-ubiquinone oxidoreductase, N001 subunit
 Species: *Xylella fastidiosa*
 Date: 18-Aug-2000
 Accession: H62811
 Sequence_revision: 20-Aug-2000
 Anonymous: 1
 Structure: 406, 151-157, 2000
 Title: The genome sequence of the orange
 Referr: The genome sequence of the orange

Sequence number: 882515; MIMD:20365717; PMID:10910347
 Note: for a complete list of authors see reference number A59328 below
 Accession: H82821
 Status: preliminary
 Molecule type: DNA
 Residues: 1-444 <SIM>
 Cross-references

Experimental source: GR/AE003884; CB/AE003849; NID:99105127; PIDN:AA683121.1; GSPDB:GCG-BJ-Stimpson, A.J.G.; Retnaach, F.C.; Attuda, P.; Abreu, F.A.; Agencio, M.; Alverenga, R.; Biondes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canabarro, L.E.A.; Catão, D.M.; Carreira Neto, E.; Docena, M.R.P.; El-Dorriy, H.; Facchinani, A.F.; Ferreira, A.U.S.; J.A.; Authors: Perreira, C.; June 2000
J.D.; Junqueira, M.L.; V.C.A.; Ferro Chado, M.A.; Madureira, K.; Kemper, E.L.; Atano, M.A.; Magalhães, J.A.; Paço, I.C.

[illegible][illegible]

-----PTGLKWSFMPKG 87

RESULT 13
 B89841
 hypothetical protein SA0652 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: B89841
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, L.; O
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
 C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: B89841
 A:Accession: B89841
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <R>
 A:Cross-references: GB:BA000018. D:
 A:Experimental:

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 : Search time 9.31811 Seconds
(without alignments)
928.727 Million cell updates/sec

Title: US-09-821-726A-13_COPY_78_119
Perfect score: 221
Sequence: 1 KKTCTVHKMKKEVMPSTIQLSL.....LVKEKKLQKGGPGPPPKGL 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: SP_archaea:*
- 2: SP_bacteria:*
- 3: SP_fungi:*
- 4: SP_human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phase:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_rvirus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64	29.0	1677	11 070373	070373 mus musculu
2	62.5	28.3	467	4 09H9F1	09H9F1 homo sapien
3	61.5	27.8	311	16 09HTC9	09htc9 pseudomomas
4	59	26.7	637	11 08R2Y1	08R2Y1 mus musculu
5	58	26.2	136	4 09H1L1	09h1l1 homo sapien
6	58	26.2	281	16 097TT2	097tt2 clostridium
7	58	26.2	707	4 09NMP3	09nmp3 homo sapien
8	58	26.2	707	4 09H5I2	09h5i2 homo sapien
9	58	26.2	862	4 09H261	09h261 homo sapien
10	58	26.2	1821	4 08WMO0	08wmo0 homo sapien
11	57.5	26.0	227	11 08R134	08r134 mus musculu
12	57.5	26.0	306	4 09NVM2	09nvm2 homo sapien
13	57.5	26.0	1582	4 09H301	09h301 homo sapien
14	57.5	26.0	1602	4 09H2T5	09h2t5 homo sapien
15	57.5	26.0	1634	4 09H314	09h314 homo sapien
16	57	25.8	438	11 099J0B1	099j0b1 mus musculu

17	57	25.8	438	11 091VC4	091vc4 mus musculu
18	57	25.8	494	5 09XZW0	09xzw0 heliothis v
19	57	25.8	496	5 018468	018468 heliothis v
20	56.5	25.6	434	6 08S001	08s001 macaca mula
21	56.5	25.6	464	5 09V8D8	09v8d8 drosophila
22	56	25.3	222	5 09V7T2	09v7t2 drosophila
23	55.5	25.1	322	13 09PTB4	09ptb4 brachydanio
24	55.5	25.1	388	16 09F339	09f339 streptomyce
25	55.5	25.1	444	16 09PGJ0	09pgj0 xyella fas
26	55	24.9	160	16 099V55	099v55 staphylococ
27	55	24.9	380	5 022948	022948 caenorhabd
28	55	24.9	494	6 08S068	08s068 sus scrofa
29	55	24.9	850	2 08VW80	08vw80 rhodococcus
30	55	24.9	1714	10 09FMM3	09fmm3 arabidopsis
31	54	24.4	438	11 09WV78	09wv78 rattus norv
32	54	24.4	468	2 09X681	09x681 clostridium
33	54	24.4	485	2 0936F0	0936f0 marinomonas
34	54	24.4	618	16 09RK22	09rk22 streptomyc
35	54	24.4	783	11 09QY56	09qy56 mus musculu
36	54	24.4	862	11 09EPY1	09epy1 mus musculu
37	54	24.4	875	2 047245	047245 escherichia
38	54	24.4	875	16 08XE30	08xe30 escherichia
39	54	24.4	880	2 054355	054355 serratia ma
40	54	24.4	891	16 08ZGR5	08zgr5 yersinia pe
41	54	24.4	996	17 058627	058627 pyrococcus
42	54	24.4	1779	11 08VDD9	08vdd9 mus musculu
43	53.5	24.2	198	16 099ZEF2	099zef2 streptococ
44	53.5	24.2	502	16 09XTU7	09xtu7 streptomyce
45	53.5	24.2	899	11 099K26	099k26 mus musculu

ALIGNMENTS

RESULT 1

ID 070373 PRELIMINARY; PRT: 1677 AA.

AC 070373:

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Xin.

GN Xin.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART MUSCLE;

RX PubMed=9159189;

RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;

RT "Differential display of mRNAs from the atrioventricular region of developing chicken hearts at stages 15 and 21.";

RL Front. Biosci. 1:al-015(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART MUSCLE;

RX MEDLINE=99146891; PubMed=10021346;

RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,

RA Krob S.L., Schultheiss T.M., Evans S., Lin J.J.-C.;

RL "Regulation of a novel gene, Xin, in cardiac morphogenesis.";

DR EMBL; AF051945; AAC06023.1; -

DR MGI; MGI:133878; Xin.

SO SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;

Query Match 29.0%; Score 64; DB 11; Length 1677;

Best local Similarity 30.6%; Pred. No. 23;

Matches 11; Conservative 10; Mismatches 3; Indels 12; Gaps 1;

QY 5 IVHKMKKEVMPSTIQLSLVKEKKLQKGGPGPPPK 40

::: :::: | :: ::|||

ID Q97TT2 PRELIMINARY; PRT; 281 AA.
AC Q97TT2;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G1P related phosphodiesterase.
GN CAP0015.
OS Clostridium acetobutylicum.
OC Clostridia: Firmicutes: Bacillus/Clostridium group: Clostridia;
OC Clostridiales: Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RA MEDLINE-21359325; PubMed-11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT *Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.*
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE01438; AAK76761.1; -
DR InterPro: IPR004129; GDDP.
DR Pfam: PF03009; GDDP: 1.
KM Plasmid; Complete proteome.
SQ SEQUENCE 281 AA; 32023 MW; A19BC118FDECA10 CRC64;

Query Match 26.2%; Score 58; DB 16; Length 281;
Best Local Similarity 36.0%; Pred. No. 21;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 1 KKTCTVHKMKKEVMPSTQSDALVK 25
DB 171 EKKCLVHSMSTYRLVQKSLDSEIK 195

RESULT 7
O9NWP3 PRELIMINARY; PRT; 707 AA.
AC O9NWP3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KAI1A571 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAL MUCOSA;
RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA Hirao M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT *NEO human cDNA sequencing project.*
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK000712; BAA91336.1; -
DR InterPro: IPR001487; Bromodomain.
DR Pfam: PF00439; bromodomain; 2.
DR PRINTS: PR00503; BROMODOMAIN.
DR SMART: SM00297; BROMO: 2.
DR PROSITE: PSS0014; BROMODOMAIN_2; 2.
SQ SEQUENCE 707 AA; 80344 MW; FB8344D6B3B15AF7 CRC64;

Query Match 26.2%; Score 58; DB 4; Length 707;
Best Local Similarity 43.6%; Pred. No. 55;
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40
DB 565 VPIRDEVLPSTCNFLSETNNVKEDLLQKKNRGGRPK 603

RESULT 8
O96H52 PRELIMINARY; PRT; 707 AA.
AC O96H52;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Pleckstrin homology domain interacting protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC008909; AAH08909.1; -
DR InterPro: IPR001487; Bromodomain.
DR Pfam: PF00439; bromodomain; 2.
DR PROSITE: PSS0014; BROMODOMAIN_2; 2.
SQ SEQUENCE 707 AA; 80287 MW; C0F903A46BB109F CRC64;

Query Match 26.2%; Score 58; DB 4; Length 707;
Best Local Similarity 43.6%; Pred. No. 55;
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40
DB 565 VPIRDEVLPSTCNFLSETNNVKEDLLQKKNRGGRPK 603

RESULT 9
O9H261 PRELIMINARY; PRT; 862 AA.
AC O9H261;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IRS-1 PH domain binding protein PHIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-20568313; PubMed-11018022;
RX Farhang-Fallah J., Yin X., Trentin G., Cheng A.M., Rozakis-Adcock M.,
RT *Cloning and Characterization of PHIP, a Novel Insulin Receptor
RT Substrate-1 Pleckstrin Homology Domain Interacting Protein.*;
RL J. Biol. Chem. 275:40492-40497(2000).
DR EMBL: AF310250; AAG45145.1; -
DR InterPro: IPR001487; Bromodomain.
DR Pfam: PF00439; bromodomain; 2.
DR PRINTS: PR00503; BROMODOMAIN.
DR SMART: SM00297; BROMO: 2.
DR PROSITE: PSS0014; BROMODOMAIN_2; 2.
SQ SEQUENCE 862 AA; 98708 MW; 76F30382C8E41F12 CRC64;

Query Match 26.2%; Score 58; DB 4; Length 862;
Best Local Similarity 43.6%; Pred. No. 67;
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;

OY 6 VHKMKKEVMPSTQSDALVK 40
DB 720 VPIRDEVLPSTCNFLSETNNVKEDLLQKKNRGGRPK 758

RESULT 10
O8WM00 PRELIMINARY; PRT; 1821 AA.
ID O8WM00

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AC 08WMQ0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE WD repeat domain 11 protein (Fragment).
GN WDR11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scott H.S., Barras C., Miltaz L., Michaud J., Guidi S., Scamuffa N.,
RA Antonarakis S.E.;
RT "Isolation and characterization of a new chromosome 21 gene, WDR9, its
RT paralogue on chromosome 6 and their murine homologues.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ303102; CAC83118.1; -
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00439; bromodomain; 2.
DR Pfam: PF00400; WD40; 8.
DR PRINTS: PRO0503; GPROTEINBRPT.
DR PRODOM: PD000018; WD40; 1.
DR SMART: SM00297; BROMO; 2.
DR SMART: SM00320; WD40; 8.
DR PROSITE: PS00614; BROMODOMAIN_2; 2.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE: PS00882; WD_REPEATS_2; 5.
DR PROSITE: PS0294; WD_REPEATS_REGION; 1.
KW WD repeat.
FT NON_TER
FT SEQUENCE 1821 AA; 266646 MW; 6A132145143C8C3 CRC64;
SQ

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```

Query Match 26.2%; Score 58; DB 4; Length 1821;
Best Local Similarity 43.6%; Pred. No. 1,4e+02;
Matches 17; Conservative 3; Mismatches 15; Indels 4; Gaps 1;
DB 1679 VHPIDGVDGLVSMGSMQPLHFGGPPPHNL 1717

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RESULT 11
08R134
ID 08R134; PRELIMINARY; PRT; 227 AA.
AC 08R134;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to polybromo 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC025605; AAH25605.1; -
FT NON_TER
FT SEQUENCE 227 AA; 24197 MW; A9C1182C840DE183 CRC64;
SQ

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```

Query Match 26.0%; Score 57.5; DB 11; Length 227;
Best Local Similarity 43.3%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
DB 14 MPSIOS-LDALVKKKLGKGGPGPPKGL 42
DB 32 LPPLOGVDGLVSMGSMQPLHFGGPPPHNL 61

```

```

RESULT 12
09NMW2
ID 09NMW2; PRELIMINARY; PRT; 306 AA.
AC 09NMW2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ10645 fis, clone NTZRP2005767, moderately similar to G.gallus
DE Pbl gene (Polybromo 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEO human cDNA sequencing project.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=DUODENUM;
RA Strausberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK001507; BAA91728.1; -
DR EMBL: BC015323; AAH15323.1; -
DR HSSP: P07155; IHMF.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF00505; HMG_box; 1.
DR SMART: SM00398; HMG; 1.
FT SEQUENCE 306 AA; 33028 MW; 649E417571F59B64 CRC64;
SQ

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Query Match 26.0%; Score 57.5; DB 4; Length 306;
Best Local Similarity 43.3%; Pred. No. 27;
Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
DB 11 LPPLOGVDGLVSMGSMQPLHFGGPPPHNL 140

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RESULT 13
09H301
ID 09H301; PRELIMINARY; PRT; 1582 AA.
AC 09H301;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BAF180.
GN BAF180.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20542072; PubMed-11078522;
RA Xue Y., Canman J.C., Lee C.S., Nie Z., Yang D., Moreno G.T.,
RA Young M.K., Salmon E.D., Wang W.;
RT "The human SWI/SNF-B chromatin-remodeling complex is related to yeast
RT Rsc and localizes at kinetochores of mitotic chromosomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:13015-13020(2000).
DR EMBL: AF197569; AAG34760.1; -
DR HSSP: P07155; IHMF.
DR InterPro: IPR001395; Aldo/ket_red.
DR InterPro: IPR001025; BAH.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR000910; HMG_12_box.
DR Pfam: PF01426; BAH; 2.
DR Pfam: PF00439; Bromodomain; 5.

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DR Pfam; PF00505; HMG_box; 1.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00439; BAH; 2.
 DR SMART; SM00297; BROMO; 6.
 DR SMART; SM00398; HMG; 1.
 DR PROSITE; PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00633; BROMODOMAIN_1; 3.
 DR PROSITE; PS50014; BROMODOMAIN_2; 6.
 SQ SEQUENCE 1582 AA; 181153 MW; 9862B959F36A4070 CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1582;
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 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLOGKGGPPPKGL 42
 DB 1387 LPPILOGPYDGLVSGMSQPLHPGPPPHHL 1416

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 O9H275 PRELIMINARY; PRT; 1602 AA.
 AC O9H275;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Polydromo-1.
 GN PBL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horikawa I., Barrett C.;
 RT "cDNA Cloning of the Human Polydromo-1 Gene on Chromosome 3p21.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF225870; AAC48939.1; -.
 DR HSSP; P07155; IHMF.
 DR InterPro; IPR001025; BAH.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR000910; HMG_12_box.
 DR Pfam; PF01426; BAH; 2.
 DR Pfam; PF00439; bromodomain; 5.
 DR Pfam; PF00505; HMG_box; 1.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00439; BAH; 2.
 DR SMART; SM00297; BROMO; 6.
 DR SMART; SM00398; HMG; 1.
 DR PROSITE; PS00633; BROMODOMAIN_1; 3.
 DR PROSITE; PS50014; BROMODOMAIN_2; 6.
 SQ SEQUENCE 1602 AA; 183689 MW; B8DA103E359A48DA CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1602;
 Best Local Similarity 43.3%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLOGKGGPPPKGL 42
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RESULT 15
 O9H314

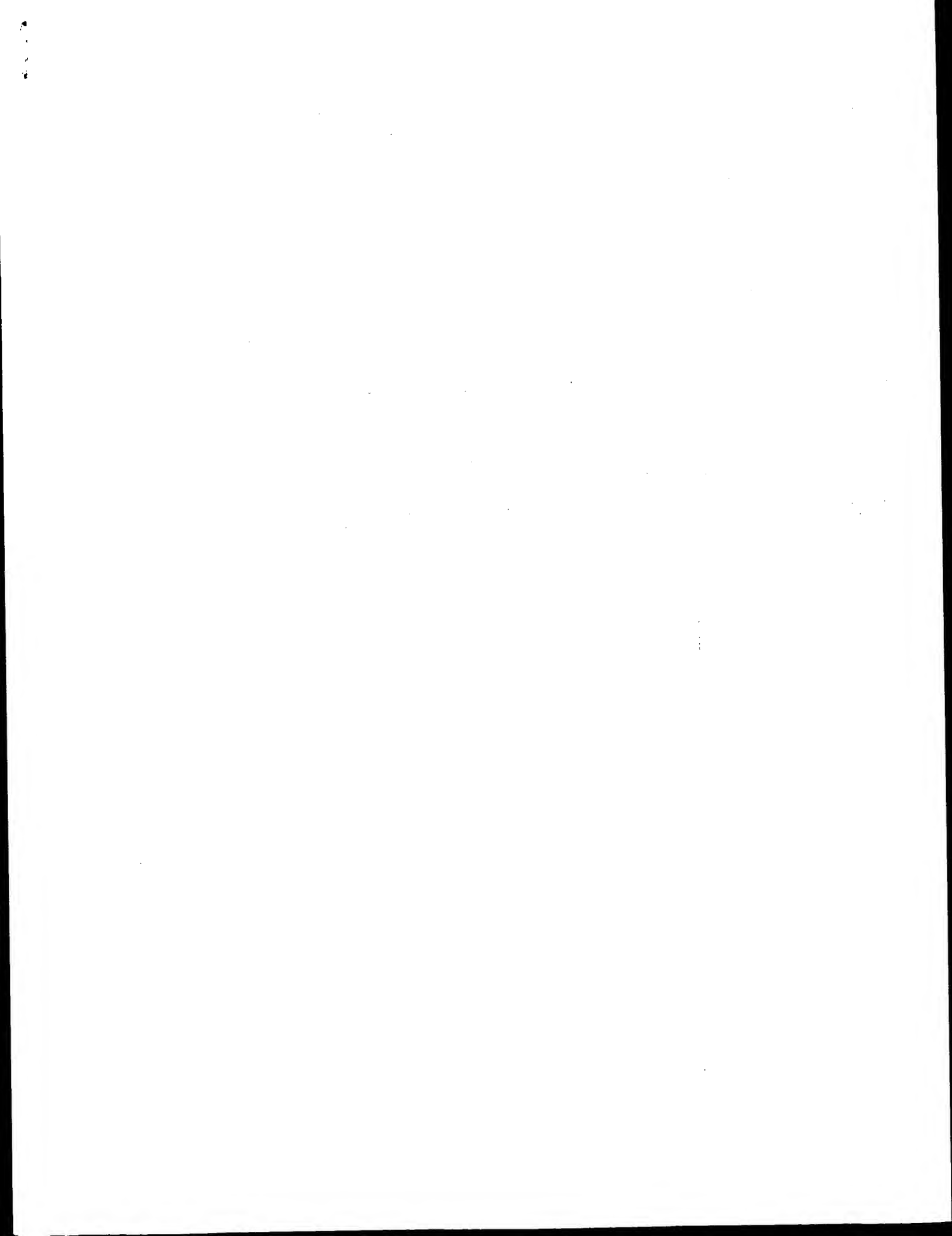
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 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Polydromo-1.
 GN PBL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horikawa I., Barrett J.C.;
 RT "cDNA Cloning of the Human Polydromo-1 Gene on Chromosome 3p21.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF177387; AAC48933.1; -.
 DR HSSP; P07155; IHMF.
 DR InterPro; IPR001395; Aldo/Ket_red.
 DR InterPro; IPR001025; BAH.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR000910; HMG_12_box.
 DR Pfam; PF01426; BAH; 2.
 DR Pfam; PF00439; bromodomain; 5.
 DR Pfam; PF00505; HMG_box; 1.
 DR PRINTS; PR00503; BROMODOMAIN.
 DR SMART; SM00439; BAH; 2.
 DR SMART; SM00297; BROMO; 6.
 DR SMART; SM00398; HMG; 1.
 DR PROSITE; PS00633; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
 DR PROSITE; PS00633; BROMODOMAIN_1; 3.
 DR PROSITE; PS50014; BROMODOMAIN_2; 6.
 SQ SEQUENCE 1634 AA; 187187 MW; FABI0935A9B8B4DD CRC64;

Query Match 26.0%; Score 57.5; DB 4; Length 1634;
 Best Local Similarity 43.3%; Pred. No. 1.5e+02;
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 14 MPSIOS-LDALVKEKKLOGKGGPPPKGL 42
 DB 1439 LPPILOGPYDGLVSGMSQPLHPGPPPHHL 1468

Search completed: April 11, 2003, 16:14:22
 Job time: 11.3181 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 : Search time 46.2966 Seconds
(without alignments)
474.899 Million cell updates/sec

Title: US-09-821-726a-18_COPY_21_185

Perfect score: 880
Sequence: 1 DYSISVNDGNSGGSGGQSV.....ISANTILWILNISFGGIAEN 165

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	687	78.1	185	AAW99667	Human secreted pro
2	687	78.1	185	AAW99667	Human secreted pro
3	687	78.1	185	AAW99667	Human secreted pro
4	687	78.1	185	AAW99667	Human secreted pro
5	687	78.1	185	AAW99667	Human secreted pro
6	687	78.1	185	AAW99667	Human secreted pro
7	687	78.1	185	AAW99667	Human secreted pro
8	687	78.1	185	AAW99667	Human secreted pro
9	687	78.1	185	AAW99667	Human secreted pro
10	687	78.1	185	AAW99667	Human secreted pro

11	687	78.1	194	AAW69974	Cancer associated
12	687	78.1	194	AAW69974	Cancer associated
13	567.5	64.5	184	AAW69974	Cancer associated
14	186	21.1	176	AAW69974	Cancer associated
15	186	21.1	184	AAW69974	Cancer associated
16	186	21.1	184	AAW69974	Cancer associated
17	185	21.0	184	AAW69974	Cancer associated
18	185	21.0	184	AAW69974	Cancer associated
19	185	21.0	184	AAW69974	Cancer associated
20	185	21.0	184	AAW69974	Cancer associated
21	185	21.0	184	AAW69974	Cancer associated
22	154.5	17.6	147	AAW69974	Cancer associated
23	94.5	10.7	95	AAW69974	Cancer associated
24	87	9.9	695	AAW69974	Cancer associated
25	81	9.2	298	AAW69974	Cancer associated
26	81	9.2	1051	AAW69974	Cancer associated
27	81	9.2	1051	AAW69974	Cancer associated
28	79.5	9.0	142	AAW69974	Cancer associated
29	79.5	9.0	501	AAW69974	Cancer associated
30	79.5	9.0	451	AAW69974	Cancer associated
31	79	9.0	380	AAW69974	Cancer associated
32	78	8.9	251	AAW69974	Cancer associated
33	78	8.9	316	AAW69974	Cancer associated
34	78	8.9	343	AAW69974	Cancer associated
35	78	8.9	349	AAW69974	Cancer associated
36	77.5	8.8	197	AAW69974	Cancer associated
37	77	8.8	181	AAW69974	Cancer associated
38	77	8.8	410	AAW69974	Cancer associated
39	77	8.8	803	AAW69974	Cancer associated
40	77	8.8	803	AAW69974	Cancer associated
41	77	8.8	803	AAW69974	Cancer associated
42	77	8.8	803	AAW69974	Cancer associated
43	77	8.8	803	AAW69974	Cancer associated
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45	77	8.8	954	AAW69974	Cancer associated

ALIGNMENTS

RESULT 1
ID AAW99667 standard; protein; 185 AA.
AAW99667
07-JUN-1999 (first entry)
Human secreted protein clone eJ90_5 protein.
Human; secreted protein; nutritional; cytokine; cell proliferation;
differentiation; immune stimulating; vaccine; haematopoiesis regulation;
tissue growth; chemotactic; chemokine; haemostatic; thrombolytic;
anti-inflammatory; cadherin; tumour invasion suppressor;
tumour inhibition; gene therapy.
Homo sapiens.
WO9907840-A1.
18-FEB-1999.
06-AUG-1998; 98W0-US16318.
04-AUG-1998; 98US-0120189.
06-AUG-1997; 97US-0906708.
(GENY) GENETICS INST INC.
Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
Merberg D, Racie LA, Steininger RJ, Treacy M;
WPI: 1999-167419/14.

KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
XX
PD 06-JAN-2000.
XX
PE 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCYTE) INCYTE PHARM INC.
XX
PI Lal P, Tang YF, Gorgone GA, Corley NC, Guegler KJ, Baughn MK;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI: 2000-160673/14.
DR N-PSDB: AA298157.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1: Page 193-194; 327pp; English.
XX
CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases), schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 185 AA:
XX
Query Match 78.1%; Score 687; DB 21; Length 185;
Best Local Similarity 73.3%; Pred. No. 1,4e-70;
Matches 121: Conservative 22; Mismatches 22; Indels 0; Gaps 0;
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DB 21 NYVINVNDGNSGSGQSVSNNEHNVANVYNNNGNSNMAALMDYRTGFAVTRLEPKKS 80
OY 61 CTVHKKKKEKMPQLDALVKEKKLQGGKGGPPPKSLKSYVNPVNDLDRFGKSLVA 120
DB 81 CTVHKKKKEKMPQLDALVKEKKLQGGKGGPPPKSLKSYVNPVNDLDRFGKSLVA 140

OY 121 MCKGIPTMAEIEQGANLISYSEKCSANILWILINISFCGIAEN 165
DB 141 MCKGIPTMAEIEQGANLISYSEKCSANILWILINISFCGIAEN 185
RESULT 4
ID AAY66686 standard; protein; 185 AA.
XX
AC AAY66686;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1005.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO963088-A2.
XX
PD 09-DEC-1999.
XX
PE 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.

PR	19-AUG-1998;	98US-0097141.
PR	20-AUG-1998;	98US-0097218.
PR	24-AUG-1998;	98US-0097661.
PR	26-AUG-1998;	98US-0097951.
PR	26-AUG-1998;	98US-0097952.
PR	26-AUG-1998;	98US-0097954.
PR	26-AUG-1998;	98US-0097955.
PR	26-AUG-1998;	98US-0097971.
PR	26-AUG-1998;	98US-0097974.
PR	26-AUG-1998;	98US-0097978.
PR	26-AUG-1998;	98US-0097979.
PR	31-AUG-1998;	98US-0098014.
PR	31-AUG-1998;	98US-0098525.
PR	16-SEP-1998;	98US-0100634.
PR	12-JAN-1999;	99US-0115565.
XX	(GETH) GENENTECH INC.	
PA		
XX		
PI	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;	
PI	Wood Wf, Yuan J;	
XX		
DR	WPLI: 2000-072883/06.	
XX	N-PSDB: AAB65023.	
PT	Membrane-bound proteins and related nucleotide sequences	-
XX	claim 12; Fig 139; 822pp; English.	
PS		
XX	The invention provides membrane-bound PRO polypeptides and	
CC	polynucleotides encoding them. The PRO sequences of the invention were	
CC	identified based on extracellular domain homology screening. The PRO	
CC	sequences have homology with proteins including LDL receptors, TIE	
CC	ligands and various enzymes. The membrane-bound proteins and receptor	
CC	molecules are useful as pharmaceutical and diagnostic agents. Receptor	
CC	immunoadhesins, for instance, can be used as therapeutic agents to block	
CC	receptor-ligand interactions. The membrane-bound proteins can also be	
CC	employed for screening of potential peptide or small molecule inhibitors	
CC	of the relevant receptor/ligand interaction. The PRO encoding sequences	
CC	are useful as hybridization probes, in chromosome and gene mapping and in	
CC	the generation of antisense RNA and DNA. PRO nucleic acid sequences	
CC	will also be useful for the preparation of PRO polypeptides, especially	
CC	by recombinant techniques.	
CC		
XX		
SQ	Sequence 185 AA;	
	Query Match 78.1%; Score 687; DB 21: Length 185;	
	Best local similarity 73.3%, Pred. No. 1.4e-70;	
	Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0	
QY	1 DYSISVNDNGSGGGQGSVSYNNEHNNAVYDNNNGWSMNLMDYRTGFAVTRLEPKS 60 ::: : : : : : : : : : :	
Dd	21 NYNINVDNDNNAGSGQGQSVSYNNEHNNAVYDNNNGWSMNSIMDWYGNGFAATRLPQKKT 80 : : : : : : : : : :	
QY	61 CIVHKMKKEAMPISLOALDALVYEKKLQCKRGCGPPPKSLRSYSNRKNVNDLKFGKSIVA 120 : : : : : : : : : :	
Dd	81 CIVHMKNEVPMSIQSLDALVYEKKLQCKRGCGPPPKGLMTYSVNPKNKYDLISKFGKNIAN 140 : : : : : : : : : :	
QY	121 MCKGIPTYMAEIIQGANLISYSEKISANIITILMLNISFCGGIAEN 165 : : : : : : : : : :	
Dd	141 MCRGIPTYMAEEMQASLFYISGTCYTTSVLMIIVDISRCGDIVEN 185 : : : : : : : : : :	
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ID	AAB65209 standard; Protein: 185 AA.	
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AC	AAB65209;	
XX		
DT	02-APR-2001 (first entry)	
XX		
XE	Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.	

Human; secreted and transmembrane protein; PRO; cytosolic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.

Homo sapiens.

WO200073454-A1.

07-DEC-2000.

30-MAR-2000; 2000WO-US08439.

02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US03565.
PR 11-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04914.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gether H, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
PI Zhang Z;

XX WPI: 2001-032160/04.
DR N-PSDB; AAF44169.
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 139; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AA44270 to AA44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

XX Sequence 185 AA;

Query Match 78.1%; Score 687; DB 22; Length 185;
Best local Similarity 73.3%; Pred. No. 1,4e-70;

Matches 121: Conservative 22: Mismatches 22: Indels 0: Gaps 0:

QY 1 DYSISYNDGSGGGGSGGSSVSYNNEHNVANVNNNGNKNALMDYRTGFAVRLPEKKS 60
DB 21 NYNINVDNNNGNAGSGGSSVSYNNEHNVANVNNNGNKNALMDYRTGFAVRLPEKKS 80
QY 61 CIVHKKKKFAMPSLQALDLVKEKKLOCKGPGGPPKSLRYSVNPKNVDLDFKGSIVA 120
DB 81 CIVHKKKKFAMPSLQALDLVKEKKLOCKGPGGPPKSLRYSVNPKNVDLDFKGSIVA 140
QY 121 MCKGIPYMAEIOGANLISYSEKCSANITLILNISFCGIAEN 165
DB 141 MCKGIPYMAEIOGANLISYSEKCSANITLILNISFCGIAEN 185

RESULT 6
AAB50957
ID AAB50957 standard; protein; 185 AA.

AC AAB50957;
XX 21-MAR-2001 (first entry)
DT
XX
XX
XX

Human PRO1005 protein.

Human; PRO; cytosolic; nocotropic; neuroprotective; respiratory general;
anti-inflammatory; antiangiogenic; immunosuppressive; immunostimulant;
PRO agonist; cancer; inflammatory disorder; immunological disorder.

Homo sapiens.

WO200073348-A2.

07-DEC-2000.

30-MAY-2000; 2000WO-US14941.

XX 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-0140650.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US30999.
PR 20-DEC-1999; 99WO-US30999.
PR 06-JAN-2000; 2000WO-US03565.
PR 11-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-0187202.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.

(GETH) GENENTECH INC.

XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff KC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;

XX WPI: 2001-016509/02.
DR N-PSDB; AAC91559.

XX Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT for treating various tumors, e.g. breast cancer, and other
PT inflammatory, angiogenic and immunological disorders -

PS Claim 31; Fig 14; 188pp; English.

XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, prostate cancer, ovarian cancer, colorectal
 CC cancer, uterine cancer, lung cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypohalamic and other glandular disorders such as neuroendocrine, stromal and
 CC disorders.

SO Sequence 185 AA:

Query Match 78.1%, Score 687, DB 22, Length 185;
 Best Local Similarity 73.3%, Pred. No. 1.4e-70;
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSISVNDGNSGGSGQSVSVNNEHNVAVDNNNGNSMNLMDYRTGFAVTRLEFKS 60
 Db 21 NYININVDNNNAGSGQSVSVNNEHNVAVDNNNGNSMNLMDYRTGFAVTRLEFKS 60
 QY 61 CIVHMKKEMPSLOALDALVKEKLGKGGPPKSLRYSVPNRVNDLKEFGKSTVA 120
 Db 81 CIVHMKKEMPSLOALDALVKEKLGKGGPPKSLRYSVPNRVNDLKEFGKSTVA 120
 QY 121 MCGIPTYMAEETIGANLISYSEKISANILMILNISFCGIAEN 165
 Db 141 MCGIPTYMAEEMQASLFEYSQTCYTSVLMIVISFCGIDVEN 185

RESULT 7
 ABB95492
 ID ABB95492 standard; Protein: 185 AA.

XX ABB95492;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO1005 SEQ ID NO: 140.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW antiarteriosclerotic; antidiabetic; antihypertensive; antineoplastic;
 OS Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23322.

XX 24-AUG-2000; 2000WO-US23322.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0664610.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806899.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODD) GODDARD P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANU) PANI J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2002-171999/22.
 DR N-PSDB; ABL95630.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 PS Claim 11: Fig 140, 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including a
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC healing. The present sequence is a PRO protein of the invention.

SO Sequence 185 AA:

Query Match 78.1%, Score 687, DB 23, Length 185;
 Best Local Similarity 73.3%, Pred. No. 1.4e-70;
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSISVNDGNSGGSGQSVSVNNEHNVAVDNNNGNSMNLMDYRTGFAVTRLEFKS 60
 Db 21 NYININVDNNNAGSGQSVSVNNEHNVAVDNNNGNSMNLMDYRTGFAVTRLEFKS 60
 QY 61 CIVHMKKEMPSLOALDALVKEKLGKGGPPKSLRYSVPNRVNDLKEFGKSTVA 120
 Db 81 CIVHMKKEMPSLOALDALVKEKLGKGGPPKSLRYSVPNRVNDLKEFGKSTVA 120
 QY 121 MCGIPTYMAEETIGANLISYSEKISANILMILNISFCGIAEN 165

25-JUL-2000; 2000US-220666P.
26-JUL-2000; 2000US-220893P.
28-JUL-2000; 2000MO-US20710.
23-AUG-2000; 2000MO-US23522.
24-AUG-2000; 2000MO-US23522.
15-SEP-2000; 2000US-000000P.
10-NOV-2000; 2000MO-US30873.
28-NOV-2000; 2000MO-US30873.
01-DEC-2000; 2000MO-US32678.
20-DEC-2000; 2000US-0747259.
20-DEC-2000; 2000MO-US34956.
28-FEB-2001; 2001MO-US06520.
10-MAY-2001; 2001US-0854280.
25-MAY-2001; 2001MO-US17092.
(GENE) GENENTECH INC.
Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL; WPI: 2002-172001/22.
N-PSDB; ABK33609.
One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -
Claim 11; Figure 148; 359pp; English.
The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression in, pericyte cells, for stimulating the release of tumour necrosis factor- α from human blood, for stimulating the release of tumour necrosis factor- α from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AA083592-AA083713 represent human PRO protein sequences of the invention.
Sequence 185 AA:
Query Match 78.1%; Score 687; DB 23; Length 185;
Best Local Similarity 73.3%; Pred. No. 1.4e-70;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
QY 1 DYSISVNDGSGGSGGQSVSYNNHNANVANDNNNGNSMNAIMDYRTGFVTRLEPKRS 60
DB 21 NYNINVNDNNAGSGGQSVSYNNHNANVANDNNNGNSMNAIMDYRTGFVTRLEPKRT 80
QY 61 CIVHMKKEAMPISQALDALVKEKKLOGKGGPPPSRLRYSVNPNVDNLDKFGKSIYA 120
DB 81 CIVHMKKEAMPISQALDALVKEKKLOGKGGPPPSRLRYSVNPNVDNLDKFGKSIYA 140
QY 121 MCKGIPTYMAEIOGANLISYSEKISANILMILINISFCGCIEN 165
DB 141 MCKGIPTYMAEIOGANLISYSEKISANILMILINISFCGCIEN 185
RESULT 10
ID AAB38329 standard; Protein; 186 AA.
AC AAB38329;
XX
XX 31-JAN-2001 (first entry)

XX
DE Human secreted protein encoded by gene 9 clone HNSAD53.
XX
XX Immunosuppressive; antiarthritic; antineumatic; antiproliferative;
XX cytoskeletal; cardiant; vasotropic; cerebroprotective; neuroprotective;
XX nontropic; antibacterial; vitricide; fungicide; ophthalmological; human;
XX vultetary; gene therapy; infection; secreted protein.
XX Homo sapiens.
XX WO200061623-A1.
XX 19-OCT-2000.
XX
XX 06-APR-2000; 2000MO-US08979.
XX
XX 09-APR-1999; 9905-0128693.
XX 26-APR-1999; 9905-0130991.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y; Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE; Young PE; WPI: 2000-647418/62.
XX
XX New nucleic acid molecules encoding 62 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives -
XX
XX Claim 11; Page 598; 716pp; English.
XX
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
XX human secreted proteins encoded by the genes AAC09512-C69587. The genes
XX and proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated from
XX a range of human tissues disclosed in the specification. The nucleic
XX acids, proteins, antibodies and (ant)agonists are useful in the
XX diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
XX rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
XX of the breast or liver; (c) cardiovascular disorders e.g. cardiac
XX arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
XX angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
XX disorders caused by bacteria, viruses and fungi; and (h) ocular
XX disorders e.g. corneal infection. The polypeptides can also be used to
XX aid wound healing and epithelial cell proliferation, to prevent skin
XX aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis.
XX
XX Sequence 186 AA:
Query Match 78.1%; Score 687; DB 21; Length 186;
Best Local Similarity 73.3%; Pred. No. 1.4e-70;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
QY 1 DYSISVNDGSGGSGGQSVSYNNHNANVANDNNNGNSMNAIMDYRTGFVTRLEPKRS 60
DB 21 NYNINVNDNNAGSGGQSVSYNNHNANVANDNNNGNSMNAIMDYRTGFVTRLEPKRT 80
QY 61 CIVHMKKEAMPISQALDALVKEKKLOGKGGPPPSRLRYSVNPNVDNLDKFGKSIYA 120
DB 81 CIVHMKKEAMPISQALDALVKEKKLOGKGGPPPSRLRYSVNPNVDNLDKFGKSIYA 140
QY 121 MCKGIPTYMAEIOGANLISYSEKISANILMILINISFCGCIEN 165
DB 141 MCKGIPTYMAEIOGANLISYSEKISANILMILINISFCGCIEN 185
RESULT 11
ID AAM69974 standard; Protein; 194 AA.
AC AAM69974;
XX
XX

PI Pan J, Smith V, Watanabe CK, Wood WT, Zhan ;
XX WPI: 2001-602746/68.
DR N-PSDB: AAS46139.
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals a
PT to screen for modulators of the compounds -
XX Claim 11: Fig 430: 774pp; English.
XX Sequences AAU2902A-AAU29328 represent PRO polypeptides of the invention
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by determining the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide primers specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX Sequence 176 AA:
SQ
Query Match 21.18; Score: 186; DB 22; Length 176;
Best Local Similarity 28.08; Prev. No. 5,6e-13;
Matches 46; Conservative 36; Mismatches 58; Indels 24; Gap 4;
OY 11 NSGSGCOOSVNNHNANVNNNGMMSWALWDYRTGFATRLFEKKSCIVHKKKEA
DB 23 NNGGNGOETVITIDNEKNATVNIHAGSSSTTTFDKYKGYASRSLRACILKMDHON
OY 71 MPST-----QALDALVEKKLGKPGCPKPSLRYSVNDPNDLDF--GKSI
DB 83 IPIPLNLQWYIVIKQALDNMFSSNKYTW-----VKYPLDSLILKDYDFLGLSP1 ?
OY 119 VAMCKGPTVMAII FOGANLISYSFKCISANILMLTINISFCGCI 162
DB 132 EKLCNHPLYKGE\FETHWVG-AGGCAKAGLILGISICADI 174
RESULT 15
ID AAY66690 standard; protein: 184 AA.
XX AAY66690;
AC AAY66690;
DT 05-APR-2000 (first entry)
DE Membrane-bound protein p0813.
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX Homo sapiens.
OS MO9963088-A2.
XX MO9963088-A2.
XX 09-DEC-1999.
PD 02-JUN-1999; 99WO-US12252.
PF 02-JUN-1999; 98US-0087607.
PR 02-JUN-1999; 98US-0087609.
PR 02-JUN-1999; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088655.
PR 09-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 10-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.

PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 02-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091978.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 10-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 18-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 31-AUG-1998; 98US-0098014.
 PR 16-SEP-1998; 98US-0098525.
 PR 12-JAN-1999; 98US-0100634.
 PR 12-JAN-1999; 98US-0115565.
 PA (GETH) GENENTECH INC.
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX
 DR N-PSDB; AAZ65029.
 XX
 PT
 PS Membrane-bound proteins and related nucleotide sequences
 XX
 PS Claim 12; Fig 149; 822pp; English.
 CC
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were

CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX
 SQ Sequence 184 AA:
 Query Match 21.1%; Score 186; DB 21; Length 184;
 Best Local Similarity 28.0%; Pred. No. 6e-13;
 Matches 46; Conservative 36; Mismatches 58; Indels 24; Gaps 4;
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 DB 31 NNGGNVOETVITNEKNTATVNIHAGSCSTTTFDYHGVIASVLSRRACFIIMKHON 90
 QY 71 MPSTL-----QALDALVKEKLLQGGKGGPPPKSLRYSVPNPNVDNDF--GKSI 118
 DB 91 IPEPLNLOWYIEKQALDNMFNSKTYT-----VKNPLESLIKVDYDFLGSPI 139
 QY 119 VAMCKGIPTYMAEEIOGANLISEKICISANIIMILNISFCGSI 162
 DB 140 EKLCKHIFLTKGEVVENTHNVG-AGGCARAGLIGIISICADI 182

Search completed: April 11, 2003, 16:11:14
 Job time : 48.2969 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2003, 16:08:13 : Search time 16.6884 Seconds
(Without alignments)
290.907 Million cell updates/sec

Title: US-09-821-726a-18_COPY_21_185

Perfect score: 880

Sequence: 1 DVSISVNDGSGSGSQGSV.....ISANLMLINISFGGIAEN 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
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3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/BackLille1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	77	8.8	803	1	US-08-158-232-10
2	77	8.8	803	1	US-08-304-626-10
3	77	8.8	803	1	US-08-316-301A-12
4	77	8.8	803	2	US-08-611-928-10
5	77	8.8	803	3	US-09-173-891-10
6	77	8.8	803	4	US-09-076-137-12
7	77	8.8	803	5	PCT-US92-03624-12
8	75	8.5	674	4	US-09-199-637A-51
9	74.5	8.5	1240	3	US-08-930-966A-4
10	74	8.4	379	1	US-08-227-108-18
11	74	8.4	379	2	US-09-073-674-18
12	74	8.4	713	4	US-09-059-584-53
13	73	8.3	817	1	US-08-381-931B-2
14	72.5	8.2	655	2	US-08-492-027A-6
15	71	8.1	412	1	US-08-313-288B-18
16	71	8.1	1025	2	US-08-530-792D-23
17	70.5	8.0	718	4	US-09-346-237-10
18	70.5	8.0	746	4	US-09-134-001C-3214
19	70.5	8.0	1026	2	US-08-530-792D-22
20	70	8.0	300	4	US-09-134-001C-4457
21	69	7.8	730	1	US-07-846-181-5
22	68	7.7	730	1	US-07-845-989-5
23	68	7.7	370	4	US-09-142-551A-4
24	67.5	7.7	396	4	US-09-142-551A-3
25	67.5	7.7	546	2	US-08-492-027A-8
26	67.5	7.7	651	2	US-08-492-027A-1
27	67	7.6	430	2	US-08-945-848-8

28	67	7.6	2391	2	US-08-446-855A-2	Sequence 2, Appl
29	67	7.6	2391	4	US-09-150-741-2	Sequence 2, Appl
30	66.5	7.6	288	4	US-08-838-207A-324	Sequence 324, App
31	66.5	7.6	334	1	US-08-241-465B-19	Sequence 19, Appl
32	66.5	7.6	334	1	US-08-241-465B-20	Sequence 20, Appl
33	66	7.5	533	1	US-08-445-586-10	Sequence 10, Appl
34	66	7.5	596	4	US-09-752-165-2	Sequence 2, Appl
35	66	7.5	978	4	US-08-897-956A-3	Sequence 2, Appl
36	65.5	7.4	542	1	US-08-701-380-2	Sequence 2, Appl
37	65.5	7.4	542	3	US-09-032-365A-13	Sequence 13, Appl
38	65.5	7.4	722	1	US-08-158-232-51	Sequence 51, Appl
39	65.5	7.4	722	2	US-08-611-928-51	Sequence 51, Appl
40	65.5	7.4	722	3	US-09-173-891-51	Sequence 51, Appl
41	65.5	7.4	747	3	US-09-035-648-18	Sequence 18, Appl
42	65.5	7.4	747	4	US-09-001-951-18	Sequence 18, Appl
43	65.5	7.4	747	4	US-08-818-829-18	Sequence 18, Appl
44	65	7.4	467	4	US-09-134-001C-3235	Sequence 3235, Ap
45	65	7.4	606	4	US-09-187-124-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-158-232-10
: Sequence 10, Application US/08158232
: Patent No. 5596071
: GENERAL INFORMATION:
: APPLICANT: Payne, Jewel
: APPLICANT: Kennedy, M. Keith
: APPLICANT: Randall, John Brooks
: APPLICANT: Meier, Henry
: APPLICANT: Wick, Heidi Jane
: APPLICANT: Fomcetrada, Luis
: APPLICANT: Schnepf, H. Ernest
: APPLICANT: Schwab, George F.
: APPLICANT: Fu, Jenny
: TITLE OF INVENTION: No. 5596071el Bacillus thuringiensis Toxins Active
: TITLE OF INVENTION: Against Hymenopteran Pests
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: USA
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/158,232
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/887,980
: FILING DATE: 22-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/797,645
: FILING DATE: 25-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/703,977
: FILING DATE: 22-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Saliwanchik, David R.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: M/SCU104.C1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 10:

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 803 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHETICAL: YES
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bacillus thuringiensis
? INDIVIDUAL ISOLATE: PS63B
? IMMEDIATE SOURCE:
? CLONE: E. COLI NM522(PMYC1642) NRRL B-18961
?
? OS-08-158-232-10

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	Best Local	Similarity	25.5%	Pred. No. 3.3		
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					Indels	28
					Gaps	9
OY	7	NDDGNSGC---	SGGOSVS	VNNENHNAN-V	VDNNNGVNSNMLW-D	YRTGFAVTRLEPKKSC 61
Db	420	NDPGLSGVQLPAPRSV	-VNAQTQIAQYTDG	ENIMWTDRSMCTLRG	CTTNCFCGRGC 478	
OY	62	IVH-----	KMKKEAMP-S	LQALDAIVKEKKI	QGGKGGEPPEKSLRY	VNPNR-VUNLDC 113
Db	479	YNNSTGYGSCNQSLPG	OKIHALYPTQTNNV	IGOSCKELSLASHI	PYDPSNNITIDKDT 538	
OY	114	EKSTVAMCKGIPT---		YMAEELQGANLIS	142	
Db	539	DSTNIVA-KGIPVEKGYA	SSCGKVEITTEIMG	ANVVLDS 577		

TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 803 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 INDIVIDUAL ISOLATE: PS63B
 IMMEDIATE SOURCE:
 CLONE: E. coli NM522(pMYC1642) NRRL B-18961

Query Match	8.8%	Score 77	DB 1	Length 803
Best Local Similarity	25.5%	Pred. No. 3,3		
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Db	420	NDPGLSGVQLPAPRSV-VNAQTQAYQYIDGENIMMTDTRSWLCTLRGYCTTNCFPGRCG	478	
Qy	62	IVH- - - - -KKKKEAMP- -SLOALDLVKKKTIQGGKPGCPPEPKSLRYSNPNR-VDNNIDK	113	
Db	479	YNNSTGYGSCNOSLPQKITHALYPTQTNNVIGOSKDLASHPIPYDLSPNNTIDDKDT	538	
Qy	114	FEKSTVAMCKGKPT- - - - -YNAEELIOGANLISYS	142	
Db	539	DSTNIVA- -KGLPVEKGYASSGQCKVEIIEWINGANAYVOLS	577	

APPLICATION NUMBER: 07/565,544
 FILING DATE: 10-AUG-1990
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/084,653
 FILING DATE: 12-AUG-1987
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/830,050
 FILING DATE: 31-JAN-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MA20CCDCD1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 803 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 INDIVIDUAL ISOLATE: PS63B
 IMMEDIATE SOURCE:
 CLONE: E. coli MMS22 (pMTC 1642) NRRL B-18961

Query Match	8.8%	Score 77;	DB 1;	Length 803;
Best Local Similarity	25.58%	Pred. No. 3.3;		
Matches	41;	Conservative	19;	Mismatches 73; Indels 28; Gaps 9;
QY	7	NDDGNSGG---	SGQOVS	VNNEHNVA--VDNNNGNNSMALM-DYRTGAVTRLPFKKSC 61
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QY	62	IVH-----	KMKRKAMP--	SLQALDALVEKKLQGGKPGCPSPKSLRYSYNPR--VDNLQK 113
Db	479	YNNSTGGE	SCNOSTPGQK	IHALYPTQTNYLGGSGKLGILLASHIPDLPSPNNTIGDKDT 538
QY	114	FGKSIVAMCK	GIPT-----	YAAEELQGANLISYS 142
Db	539	DSTNIVA--	KQIPVEKGYASSGQK	VEITLRREVIINGANVQLS 577

RESULT 4
US-08-611-928-10
Sequence 10, Application US/08611928
Patent No. 5824792
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meier, Henry
APPLICANT: Uick, Heidi Jane
APPLICANT: Foncetrada, Luis
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SPOUNCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL

```

1 COUNTRY: USA
2 ZIP: 32606
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC Compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: PatentIn Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/611,928
11 FILING DATE: 06-MAR-1996
12 CLASSIFICATION: 530
13
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/158,232
16 FILING DATE: 24-NOV-1993
17 APPLICATION NUMBER: US 07/887,980
18 FILING DATE: 22-MAY-1992
19 CLASSIFICATION: 530
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/797,645
23 FILING DATE: 25-NOV-1991
24 CLASSIFICATION: 530
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/703,977
28 FILING DATE: 22-MAY-1991
29 CLASSIFICATION: 530
30
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Salliwachik, David R.
33 REGISTRATION NUMBER: 31,794
34 REFERENCE/DOCKET NUMBER: M/SCJ104.C1
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 904-375-8100
37 TELEFAX: 904-372-5680
38
39 INFORMATION FOR SEQ ID NO: 10:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 803 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: protein
46 HYPOTHEetical: YES
47
48 ANTI-SENSE: NO
49 ORIGINAL SOURCE:
50 ORGANISM: Bacillus thuringiensis
51 INDIVIDUAL ISOLATE: PS63B
52 IMMEDIATE SOURCE:
53 CLONE: E. coli M5622(pMTc1642) NRRL B-18961
54
55 US-08-611-928-10

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Query Match      8.8%; Score 77; DB 2; Length 803;
Best Local Similarity 25.5%; Pred. No. 3.3;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

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Db 420 NDPGSGVQVLPAPKPSV-VNAQOTAOYTTDGENITPTDGRSGLCTLRGCTTNCFPRGC 478
OY 62 IVH-----KMKKEAMP--SLQALDALVEKKLOGKGPGPPKSLRYSVNPAPR-VDNLDP 113
Db 479 YNNSTGYCSENGNSLPGQKIHALVPFQTNVLGSGSKIGLLASHLPYDLSPPANTTIGDKPT 538
OY 114 FGKSIVAMCKGIPF-----VYAEELIGCANLISYS 142
Db 539 DSTNIVA--KGIPEKGYASSGQKVEILIREWINGANVQLS 577

RESULT 5
US-09-173-891-10
; Sequence 10, Application US/09173891
; Patent No. 6077937
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Kennedy, M. Keith
; APPLICANT: Randall, John Brooks

```

APPLICANT: Meier, Henry
APPLICANT: Vick, Heidi Jane
APPLICANT: Foncecrada, Luis
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 6077937e1 Bacillus thuringiensis Toxins Active
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,232
FILING DATE:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
APPLICATION NUMBER: US 07/703,977
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanichik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SC104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: PS63B
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMVC1642) NRRL B-18961
US-09-173-891-10
Query Match 8.8%; Score 77; DB 3; Length 803;
Best Local Similarity 25.5%; Pred. No. 3.3;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

DB 539 DSTNIVA--KGIPVEKGYASSGQKVEILIREWINGANVOLS 577
RESULT 6
US-09-076-137-12
Sequence 12, Application US/09076137B
Patent No. 6165195
GENERAL INFORMATION:
APPLICANT: Schnepf, Harry E.
APPLICANT: Payne, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncecrada, Luis
TITLE OF INVENTION: No. 6165195e1 Nematode-Active Toxins and Genes Which Code
TITLE OF INVENTION: Therefor
FILE REFERENCE: MA-20CCD2
CURRENT APPLICATION NUMBER: US/09/076,137B
CURRENT FILING DATE: 1998-05-12
EARLIER APPLICATION NUMBER: 08/316,301
EARLIER FILING DATE: 1994-09-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 12
LENGTH: 803
TYPE: PRT
ORGANISM: Bacillus thuringiensis
US-09-076-137-12
Query Match 8.8%; Score 77; DB 4; Length 803;
Best Local Similarity 25.5%; Pred. No. 3.3;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;
DB 539 DSTNIVA--KGIPVEKGYASSGQKVEILIREWINGANVOLS 577
RESULT 7
PCT-US92-03624-12
Sequence 12, Application PC/TUS9203624
GENERAL INFORMATION:
APPLICANT: Schnepf, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncecrada, Luis
TITLE OF INVENTION: Novel Nematode-Active Toxins and Genes
TITLE OF INVENTION: Which Code Therefor
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanichik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03624
FILING DATE: 19920501
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA20C2C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-372-5800
TELEFAX: 904-375-8100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 803 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
INDIVIDUAL ISOLATE: PS63B
IMMEDIATE SOURCE:
CLONE: E. coli NM522(pMYC 1642) NRRL B-18961
PCT-US92-03624-12

Query Match 8.8%; Score 77; DB 5; Length 803;
Best Local Similarity 25.5%; Pred. No. 3.3;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;

QY 7 NDDGNSCG---SGQOSVSYNNEHNVAN-VDNNGMNSMNAIM-DYRTGFAVTRLEKKSC 61
DB 420 NDRGLSGDVLPAPMSV-VNAQTQATQYTDGENTWDTGRSWLCTLRGLSPNNTIGDKDT 478
QY 62 IVH-----KMKREAMP---SLQALDALVKEKTKLOGKGGPGPPKSLRYSVNPBR-VDNLDK 113
DB 479 YNNSYGVGSCQSILPGQKTHALYPTQYNNVLGQSGKGLSLASHIPYDLSPPNNTIGDKDT 538
QY 114 FCKSIAMCKGIP-----YMAEIIQGANLISYS 142
DB 539 DSTNIYA--KGIPVEKGVASSQKVELIREWINGANVVOQLS 577

RESULT 8
US-09-199-637A-51
Sequence 51, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 674
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-51

Query Match 8.5%; Score 75; DB 4; Length 674;
Best Local Similarity 23.1%; Pred. No. 4.4;
Matches 33; Conservative 24; Mismatches 56; Indels 30; Gaps 5;

QY 12 SGSGGQGSV-----SYNNEHNVANDNNNG--WNSMNAIMDYRTGFAV 52

DB 418 AGSGGQPIRIYNDYTRAGYNLLTSRVNDSSSVSATCNCNLTVCNTWSSPOE-AAAFAT 476
QY 53 TRLEKSCSIVHKMKREAMPISQALDALYK---KKLOGKGGPGPPKSLRYSVNPBRVD 109
DB 477 RVIGEOOQOTCEGCKQTVTAAGVGLPPLIQETYYDKKLSL-----QLLSKSRPLTAE 529
QY 110 NLDKFGKSIYAMCKGIPYMAEE 132
DB 530 NLAAGTDALPITRGVIEALRDE 552

RESULT 9
US-08-930-996A-4
Sequence 4, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLOHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-4

Query Match 8.5%; Score 74.5; DB 3; Length 1240;
Best Local Similarity 24.4%; Pred. No. 12;
Matches 33; Conservative 19; Mismatches 50; Indels 33; Gaps 6;

QY 34 NNGMNSMNAI-----WDRYTGFAVTRLEKKSCIVHKMKREAMP---SLQALDALYK 83
DB 284 NQVYNMDELNRNRYFGDGSKIYV---TRKDSVALMGNGDISMNSTEASWSLQOR 340
QY 84 KLOGKGGPGPPKSLRYSVNPBRVNDLDFKSIYAMCKGIPYMAEIIQGANLISYS 143
DB 341 HAFENMDPMGH-----SELEVGROIAPKCKGLP--LALKTAGMLRSKSE 384
QY 144 ----KCSANIITWL 154
DB 385 VERKCLIRSEIWL 399

RESULT 10

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert Company
STREET: 2800 Plymouth Road
CITY: Ann Arbor
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 5072-D1-66-TWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-073-674-18

Query Match
Best Local Similarity 23.1%; Pred No. 2.5;
Matches 51; Conservative 30; Mismatches 66; Indels 74; Gaps 13

QY 6 VNDG-----NSGSGGQGSVSNNEH-----VANVDNN-----G 36
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 33 VVEDGYILEVNRIPYKKNNGRQPV-VFLDGLLASAMWISLNLAFIADG 91
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 37 NWS-----NALMDYRTGFAVTRLEPKKSCITYHKKKKEAMPSLQALDAVKE--KKLOG 88
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 YGVWLGNNGNTWYSRNLNLYSPDSVEFWAFSPDEMAKYDLP--TIDFVKEGTGQEKLY 149
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 89 KPPG-GPPPKSLRYSVNPVRVDNL-----KEGSIYAMCKGIPTMADEIOGA 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 150 VCHSGGTIGTAFSTNPRLAERITFYALAPVATVYKTSLVNKLRLPTPTWKITFG- 208
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 137 NLSY-----SEK-----ISANILMIINISFCG 160
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 DKITYPHNFDFQIATQVCSRETLNVICSNALFI-----CG 245

RESULT 12
US-09-584-53
Sequence 53, Application US/09059584
Patent No. 6440701
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario

```

COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-059-584-53

Query Match 8.4%; Score 74; DB 4; Length 713;
Best Local Similarity 29.0%; Pred. No. 6.2;
Matches 42; Conservative 16; Mismatches 53; Indels 34; Gaps 8;

QY 10 GNSGSGGQGSVYVNEHNV-ANVDNNNGMSNMLDYRTGFAVTRLFEKKSCTVHKMK 67
DB 48 GNTGGTG-----STDVWNGANGANGSGNAGNSGNA--NSGTGSANTPEPKYQVPIIDKME 101
QY 68 KRAMSLQ-ALDALVKEKKLOGKGGPPKSLRYSVNRVDNLDK-----FGKSIAM- 121
DB 102 KQVSSIOEPAMGYAMELKLRAHP-----LNPNKKKEAKERIALDQKDLVAVE 150
QY 122 --CKGIPTMAEIOGANLISYSEK 144
DB 151 GDLTNIPF-----DKNLIETLKK 168

RESULT 13
US-08-381-931B-2
Sequence 2, Application US/08381931B
Patent No. 5714377
GENERAL INFORMATION:
APPLICANT: Tanner, Widmar, et al.
TITLE OF INVENTION: Modified fungal cells and method for
TITLE OF INVENTION: Producing recombinant products.
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,931B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 817 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-381-931B-2

Query Match 8.3%; Score 73; DB 1; Length 817;
Best Local Similarity 23.5%; Pred. No. 10;
Matches 27; Conservative 23; Mismatches 39; Indels 26; Gaps 5;

QY 38 NSNMLMDYRTGFAVTRLFEKKSCTVHKMKRAMPSLOALDALVKEKKLOGKGGPPPK 97
DB 721 SQWLSGMDYNGNTYFSSLEFKNOTL--TKRESOP---AAVSTVEETIFEDG----- 768
QY 98 SLRYSVNRVDNLDKFGKSIAMCKG-----IPTMAEIOGANLISYSEKTI 146
DB 769 -----PSYEDLNMEDGKKIFKDEGNEIDPEVVKMKLEB-EGANILVKKRAV 815

RESULT 14
US-08-492-027A-6
Sequence 6, Application US/08492027A
Patent No. 5912333
GENERAL INFORMATION:
APPLICANT: Suzuki, Shoichi
APPLICANT: Burnell, James N
TITLE OF INVENTION: DNA Encoding Carbonic Anhydrase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/492,027A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-492-027A-6

Query Match 8.2%; Score 72.5; DB 2; Length 655;
Best Local Similarity 23.4%; Pred. No. 8.3;
Matches 33; Conservative 25; Mismatches 58; Indels 25; Gaps 7;

QY 34 NGNNSNMLMDYRTGFAVTRLFEKKSCTVHKMKRAMPSLOALDALVKEKKLOGKGP-- 91
DB 435 SSGWPH---YDFVKGQGVF--WEPPDAILERLTS-----GQOQKRVNVYDKKPELFGPLK 484
QY 92 GGPPPKSLRYSVNRVDNLDKFG-----KSIAMCKGIPTMAEIOG-ANLISY 141

DB 485 SGQAFKTYMVFACSDSRVSPSVTLGLQPGFAFTVNRIAM---VPGYDKTKYTGIGSALEY 541

OY 142 SEKCISANILMLINISFOCGI 162

DB 542 AVCALKEVELLVIGHSCCGI 562

RESULT 15

US-08-313-288B-18

; Sequence 18, Application US/08313288B

; Patent No. 5750502

; GENERAL INFORMATION:

; APPLICANT: Jessell, Thomas M. and Avihu Klar

; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A

; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,288B

; FILING DATE: January 5, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28, 678

; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; TELEX:

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 412 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-313-288B-18

Query Match 8.1%; Score 71; DB 1; Length 412;

Best Local Similarity 24.1%; Pred. No. 6.4;

Matches 27; Conservative 14; Mismatches 25; Indels 46; Gaps 5;

OY 3 SISVNDG--NSGSGGQSVSVNNEHNAVNNNGNSWALMDYRTGFAVTRLEFKS 60

DB 71 SLGENDGNNNGNDGREG-----KDEDKRDGNNEDN----- 102

OY 61 CIYHKKMKKEMPSIQALDALYKEKKIOGKGGPPKSLRYSVNPNDNL 112

DB 103 ---EKLKRP-----KHKKLKOPGDGNDPDPNA-NPVPDPNPNPNVD 138

Search completed: April 11, 2003, 16:16:43

Job time: 19.6884 secs

Mon Apr 14 14:02:19 2003

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: April 11, 2003, 16:06:33 ; Search time 6.45351 Seconds
(without alignments)
474.899 Million cell updates/sec

Title: US-09-821-726A-2
Perfect score: 125
Sequence: 1 LDTWVKEOKGKPGGAPPKDLMY 23

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Maximum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_101002: *
2: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1981.DAT: *
3: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1982.DAT: *
4: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1983.DAT: *
5: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1984.DAT: *
6: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1985.DAT: *
7: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1986.DAT: *
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9: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA1988.DAT: *
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21: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA2000.DAT: *
22: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT: *
23: /SID2/gcgcdata/geneseq/geneseqp-emb1/AA2002.DAT: *

SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description
1	103	82.4	184 23 ABP09922	Human ORFX protein
2	90	72.0	185 21 AAM99667	Human secreted pro
3	90	72.0	185 21 AAB24067	Human PRO1005 prot
4	90	72.0	185 21 AAY66686	Human signal pepti
5	90	72.0	185 21 AAB52309	Membrane-bound pro
6	90	72.0	185 22 AAB50957	Human PRO1005 (UNQ
7	90	72.0	185 23 AAB5492	Human PRO1005 prot
8	90	72.0	185 23 AAB54986	Human angiogenesis
9	90	72.0	185 23 AAB54986	Human PRO1005 prot
10	90	72.0	185 23 AAB53655	Human PRO protein,

11	90	72.0	186 21 AAB38329	Human secreted pro
12	90	72.0	194 19 AAM69974	Cancer associated
13	90	72.0	194 19 AAY76591	Human ovarian tumor
14	90	72.0	194 19 AAB59646	Drosophila melanog
15	90	43.2	1194 22 AAB78655	Human UBC/CDC34 p
16	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
17	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
18	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
19	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
20	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
21	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
22	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
23	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
24	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
25	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
26	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
27	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
28	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
29	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
30	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
31	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
32	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
33	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
34	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
35	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
36	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
37	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
38	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
39	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
40	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
41	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
42	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
43	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
44	90	40.8	298 20 AAR73977	Human UBC/CDC34 p
45	90	40.8	298 20 AAR73977	Human UBC/CDC34 p

ALIGNMENTS

RESULT 1	ABP09922	standard; protein: 184 AA.
ID	ABP09922	
AC	ABP09922	
XX	24-JUN-2002 (first entry)	
DE	Human ORFX protein sequence SEQ ID NO:19826.	
XX	Human: open reading frame; ORFX: gene therapy; cancer; cirrhosis;	
KW	hyperproliferative disorder; peritonsillar; benign tumor; haemorrhage;	
KW	degenerative disorder; osteoarthritis; neurodegenerative disorder;	
KW	cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;	
KW	hypertension; hypothyroidism; cholesterol ester storage disease;	
KW	immune deficiency; immune disorder; infectious disease;	
KW	immune deficiency; immune disorder; infectious disease;	
KW	myasthenia gravis.	
CS	Homo sapiens.	
XX	WO200192523-A2.	
PN	06-DEC-2001.	
XX	29-MAY-2001; 2001WO-US10836.	
XX	30-MAY-2000; 2000US-206132P.	
PK	29-AUG-2000; 2000US-228716P.	
PR	(CURA-) CURAGEN CORP.	
XX	Shinketsu RA, Leach MD;	
XX		
PI		

WPL; 2002-106308/14.
N-PSDB; ABN25674

novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -

19826; 1037pp; English.

CC (referred to as open reading frame, ORF, in the specification). ABN15762 to ABN21255 encode the human ORF
CC proteins given in ABP00010 to ABP11500. ORF proteins are useful for
CC disorder or preventing a pathology associated with an ORF-associated
CC syndrome associated with ORF-associated disorder. ORF polypeptide
CC sequences can be used in gene therapy. ORF sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, hemorrhage,
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, systemic
CC arthritis, autoimmune disorders such as asthma, sclerosis, infectious
CC disease and autoimmune thyroiditis, myasthenia gravis, rheumatoid
CC disease and autoimmune inflammatory eye disease, ORF proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, for treating osteoporosis, and for gut
CC protection or regeneration and peridontal disease, and for gut
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC Sequence 184 to 222

Query Match	82.48;	Score 103;	DB 23;	Length 184;
Best Local Similarity	82.68;	Pred. No. 2.4e-07;		
Matches	13;	Conservative		

		2:	mismatches	2:	Indels	0:	Gaps	0:
97	LDPLVKKQKGGKGPGASPKDLMY	119	LDPLVKEOKGKGGAPPKDLMY	23				
	:		:					
2y								

RESULT 2
AAW99667
AAW99667 standard; Protein; 185 AA.

07-JUN-1999 (first entry)
Human secreted protein clone ej90_5 protein.
Human; secreted protein

differentiation; protein; stimulatory; cytokine; cell proliferation; tissue growth; chemotactic; chemokine; haematopoiesis regulation; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy.

WO9907840-A1.
18-FEB-1999.

06-AUG-1998; 98WO-US16318.
04-AUG-1998; 98US-0130189.
06-AUG-1997; 97US-0906708.

XX
PA
XX (GEM) GENETICS INST INC.

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM,
PI Merberg D, Raie LA, Steininger RJ, Treacy M,
XX WPI, 1999-167419/14.
OR N-PSDB; AAX19493.
OR

Claim 34: Page 98-99: 107new - New polynucleotides encoding secreted human proteins - derived from fetal kidney, adult testes, adult brain, adult heart, adult placenta or adult retina cDNA libraries

The present sequence represents a human secreted protein. The secreted protein can have activities such as: nutritional activity, cell proliferation/differentiation activity, cytokine and tissue growth activity, immune stimulating activity, haematopoietic activity, etc. (100% English).

chemokine activity, activating/inhibin activity, chemotactic activity, ligand activity, haemostatic activity and thrombolytic activity, suppressor activity, anti-inflammatory activity, chemotactic activity, protein polynucleotides and proteins activity, cadherin/tumour invasion activities which would make them suitable candidates for the amelioration of cancer.

Sequence 185 AA;
polynucleotides are also stated to be useful for gene therapy.

```

1 LDYWKREOK--GKSGGAPKDLWY 23
  ||:|||||  |||  |||  |||
97 LDALVKEKKLQGGKGGGPPPPC 100
  |||||  |||||  |||||  |||||

```

1 LDYWKREOK--GKSGGAPKDLWY 23
 97 LDALVKEKKLQGGKGGGPPPPC 100

Similarity 72.0%;
 Conservative 2; Mismatches 3; Indels 2; Gaps 1

Prox 90; DB 20; Length 185;
 Pred. 05;

LT 3
067
AAB24067 standard; Protein; 185 AA.

AA024067;
29-JAN-2001 (first entry)
Human PRO1005 protein sequ

Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth; proliferation; neurogenesis; identification; cancer; cytostatic; immunoprotective; antiinflammatory; leukæmia; lymphoid neoplasia; neuronal disorder; glial disorder; lymphoid neoplasia.

Homo sapiens.
immunologic disorder.

JAN-2000; 2000WO-US00376.

MAR-1999;	99WO-US05028.
JUN-1999;	99WO-US12252.
JUN-1999;	99US-0141037.
JUL-1999;	99US-0143048.
OCT-1999;	99US-0145698.
NOV-1999;	

99WO-US28313.
99WO-US30917

XX OS Homo sapiens.
 XX PN WO9963088-A2.
 XX PD 09-DEC-1999.
 XX PF 02-JUN-1999; 99WO-US12252.
 XX PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 03-JUN-1998; 98US-0087759.
 PR 04-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
 PR 04-JUN-1998; 98US-0088025.
 PR 04-JUN-1998; 98US-0088028.
 PR 04-JUN-1998; 98US-0088029.
 PR 04-JUN-1998; 98US-0088030.
 PR 04-JUN-1998; 98US-0088033.
 PR 04-JUN-1998; 98US-0088036.
 PR 05-JUN-1998; 98US-0088167.
 PR 05-JUN-1998; 98US-0088202.
 PR 05-JUN-1998; 98US-0088212.
 PR 05-JUN-1998; 98US-0088217.
 PR 09-JUN-1998; 98US-0088655.
 PR 10-JUN-1998; 98US-0088722.
 PR 10-JUN-1998; 98US-0088730.
 PR 10-JUN-1998; 98US-0088734.
 PR 10-JUN-1998; 98US-0088738.
 PR 10-JUN-1998; 98US-0088740.
 PR 10-JUN-1998; 98US-0088741.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-JUN-1998; 98US-0088810.
 PR 10-JUN-1998; 98US-0088811.
 PR 10-JUN-1998; 98US-0088824.
 PR 10-JUN-1998; 98US-0088825.
 PR 11-JUN-1998; 98US-0088826.
 PR 11-JUN-1998; 98US-0088858.
 PR 11-JUN-1998; 98US-0088861.
 PR 11-JUN-1998; 98US-0088863.
 PR 12-JUN-1998; 98US-0088876.
 PR 12-JUN-1998; 98US-0089090.
 PR 16-JUN-1998; 98US-0089440.
 PR 16-JUN-1998; 98US-0089512.
 PR 17-JUN-1998; 98US-0089514.
 PR 17-JUN-1998; 98US-0089532.
 PR 17-JUN-1998; 98US-0089538.
 PR 17-JUN-1998; 98US-0089598.
 PR 17-JUN-1998; 98US-0089599.
 PR 17-JUN-1998; 98US-0089600.
 PR 18-JUN-1998; 98US-0089653.
 PR 18-JUN-1998; 98US-0089801.
 PR 18-JUN-1998; 98US-0089907.
 PR 19-JUN-1998; 98US-0089947.
 PR 19-JUN-1998; 98US-0089948.
 PR 22-JUN-1998; 98US-0089952.
 PR 22-JUN-1998; 98US-0090252.
 PR 23-JUN-1998; 98US-0090254.
 PR 23-JUN-1998; 98US-0090349.
 PR 24-JUN-1998; 98US-0090355.
 PR 24-JUN-1998; 98US-0090429.
 PR 24-JUN-1998; 98US-0090431.
 PR 24-JUN-1998; 98US-0090435.
 PR 24-JUN-1998; 98US-0090444.
 PR 24-JUN-1998; 98US-0090445.
 PR 24-JUN-1998; 98US-0090461.
 PR 24-JUN-1998; 98US-0090472.
 PR 24-JUN-1998; 98US-0090535.
 PR 24-JUN-1998; 98US-0090538.
 PR 24-JUN-1998; 98US-0090540.

PR 24-JUN-1998; 98US-0090557.
 PR 25-JUN-1998; 98US-0090676.
 PR 25-JUN-1998; 98US-0090678.
 PR 25-JUN-1998; 98US-0090688.
 PR 25-JUN-1998; 98US-0090690.
 PR 25-JUN-1998; 98US-0090691.
 PR 25-JUN-1998; 98US-0090694.
 PR 25-JUN-1998; 98US-0090695.
 PR 26-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 02-JUL-1998; 98US-0091544.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 07-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 11-AUG-1998; 98US-0096012.
 PR 12-AUG-1998; 98US-0096143.
 PR 17-AUG-1998; 98US-0096146.
 PR 17-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 18-AUG-1998; 98US-0096895.
 PR 18-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 19-AUG-1998; 98US-0096960.
 PR 19-AUG-1998; 98US-0097122.
 PR 20-AUG-1998; 98US-0097141.
 PR 24-AUG-1998; 98US-0097218.
 PR 26-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 31-AUG-1998; 98US-0098014.
 PR 16-SEP-1998; 98US-0098525.
 PR 12-JAN-1999; 98US-0100634.
 XX 99US-0115565.

PD 07-DEC-2000.
 XX 30-MAY-2000; 2000WO-US14941.
 XX 02-JUN-1999; 99WO-US12252.
 XX 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000WO-US07202.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 XX (GETH) GENENTECH INC.
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 DR WPI: 2001-016509/02.
 DR N-PSDB: AAC91559.
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocellic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA:
 Query Match 72.0%; Score 90; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 2e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 Oy 1 LPTMYEOK--GKPGGAPKDLAY 23
 Db 97 LDALYKELKLGKPGGPPPKGLMY 121
 ID ABB95492 standard; Protein; 185 AA.
 AC ABB95492;
 XX 19-JUL-2002 (first entry)
 DE Human angiogenesis related protein PRO1005 SEQ ID NO: 140.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytosatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS WO200208284-A2.
 PN 31-JAN-2002.
 XX 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23328.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001US-0802706.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONTI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI: 2002-171999/22.

OS Homo sapiens.
 XX WO200208288-A2.
 PN
 XX
 XX
 PD 31-JAN-2002.
 PF 29-JUN-2001: 2001WO-US21066.
 XX
 XX 20-JUL-2000: 2000US-219556P.
 PR 25-JUL-2000: 2000US-220585P.
 PR 25-JUL-2000: 2000US-220605P.
 PR 25-JUL-2000: 2000US-220607P.
 PR 25-JUL-2000: 2000US-220624P.
 PR 25-JUL-2000: 2000US-220638P.
 PR 25-JUL-2000: 2000US-220664P.
 PR 25-JUL-2000: 2000US-220666P.
 PR 26-JUL-2000: 2000US-220833P.
 PR 28-JUL-2000: 2000WO-US20710.
 PR 23-AUG-2000: 2000WO-US23322.
 PR 24-AUG-2000: 2000WO-US23328.
 PR 15-SEP-2000: 2000US-000000P.
 PR 10-NOV-2000: 2000WO-US30873.
 PR 28-NOV-2000: 2000US-253646P.
 PR 01-DEC-2000: 2000WO-US32678.
 PR 20-DEC-2000: 2000US-0747259.
 PR 20-DEC-2000: 2000WO-US34956.
 PR 28-FEB-2001: 2001US-US06520.
 PR 10-MAY-2001: 2001WO-US054280.
 PR 25-MAY-2001: 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Carney AB, Smith V, Stephan JF, Watanabe CK, Wood WI;
 DR N-PSDB: ABK33609.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 DR
 XX
 PS Claim 11: Figure 148: 359pp: English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.
 CC
 XX
 SQ Sequence 185 AA:

Query Match 72.0%; Score 90; DB 23; Length 185;
 Best Local Similarity 72.0%; Pred. No. 2e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTMWKEOK--GKPGGAPPKDLMY 23
 ||:||||:| ||||| |||||
 Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

RESULT 11
 ID AAB38329 standard; Protein: 186 AA.
 XX
 XX
 AC AAB38329;
 XX
 XX
 DT 31-JAN-2001 (first entry)
 XX
 XX Human secreted protein encoded by gene 9 clone HNSAD53.
 DE
 XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 XX cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
 KW nocrotropic; antibacterial; virucide; fungicide; optalmalogical; human;
 KW vulnerable; gene therapy; infection; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200061623-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000: 2000WO-US08979.
 XX
 PR 09-APR-1999: 99US-0128693.
 PR 26-APR-1999: 99US-0130991.
 XX
 PA (HUMAN-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX
 DR WPI: 2000-647418/62.
 XX
 PT New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 DR
 XX
 PS Claim 11: Page 598: 716pp: English.
 XX
 CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. cardiac
 CC of the breast or liver; (c) cardiovascular disorders e.g. cerebral ischemia; (e)
 CC arrest; (d) cerebrovascular disorders e.g. Alzheimer's disease; (g)
 CC angiogenesis; (f) nervous system disorders and fungi; and (h) ocular
 CC infections caused by bacteria, viruses and fungi. The polypeptides can also be used to
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 CC
 XX
 SQ Sequence 186 AA:

Query Match 72.0%; Score 90; DB 21; Length 186;
 Best Local Similarity 72.0%; Pred. No. 2e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 LDTMWKEOK--GKPGGAPPKDLMY 23
 ||:||||:| ||||| |||||
 Db 97 IDALVKEKKLOGKGGPPPKGLMY 121
 RESULT 12
 AAM69974
 ID AAM69974 standard; Protein: 194 AA.

XX	AAW69974:	16-NOV-1998 (first entry)
AC		Cancer associated protein.
XX		Cancer: PCR: Northern blotting: ribonuclease protection assay;
XX		diagnosis; metastatic cancer.
XX		Synthetic.
XX	WO9837187-A1.	
XX	27-AUG-1998.	
XX	18-FEB-1998; 98WO-JP00667.	
XX	21-FEB-1997; 97JP-0052508.	
XX	(TAKI) TAKARA SHUZO CO LTD.	
XX	Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;	
XX	WPI: 1998-467552/40.	
XX		Detection of cancer cells in tissue samples - by changes in mRNA
XX		expression compared to normal tissue of specific cancer-associated
XX		gene sequences
XX	Claim 14; Page 64-65; 92pp; Japanese.	
XX		The cancer associated proteins AAW69974-W69976 where used in the method
XX		of the invention to detect cancer cells in tissue samples or biological
XX		fluids. They are detected by monitoring the change in mRNA expression
XX		as compared to normal tissue of one or more cancer-associated genes
XX		whose cDNA stringently hybridises to cancer associated gene nucleic acid
XX		fragments. The change in expression may be an increase or a decrease
XX		compared to normal tissue. The mRNA expression may be determined by
XX		PCR, Northern blotting or ribonuclease protection assay, or by
XX		determining the change in the amount of protein encoded by the gene(s) as
XX		compared to normal tissue, for example by using a labelled antibody
XX		recognising the protein. Detection of cancer cells for cancer diagnosis,
XX		including detection of metastatic cancer cells in tissues other than the
XX		primary tumour site.
XX	Sequence 194 AA:	
XX		
XX	Query Match 72.0%; Score 90; DB 19; Length 194;	
XX	Best Local Similarity 72.0%; Pred. NO. 2.1e-05;	
XX	Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;	
XX	1 LDTWKEQK--GKGPGAGPKDLMY 23	
XX	: :	
XX	106 LDALVKEKKLOGKGGPGPPKGLMY 130	
XX		
XX	RESULT 13	
XX	AAV76591	
XX	ID AAV76591 standard; Protein; 194 AA.	
XX	AAV76591;	
XX	10-APR-2000 (first entry)	
XX		
XX	Human ovarian tumor EST fragment encoded protein 87.	
XX		
XX	Expressed sequence tag; EST; human; ovarian tumor; anticancer;	
XX	gene therapy; treatment.	
XX		
XX	Homo sapiens.	
XX		
XX	DE19817557-A1.	

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XX          21-OCT-1999.
PD
PF          09-APR-1998;    98DE-1017557.
XX
XX          09-APR-1998;    98DE-1017557.
PR
PA          (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI          Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
XX          WPI; 1999-591920/51.
DR
XX          N-Psdb; AAZ77487.
PT
PT          New nucleic acid sequences expressed in ovarian, and some other, cancer
PT          tissues, and derived polypeptides, for treatment of ovarian cancer and
PT          identification of therapeutic agents .
PS
PS          Claim 25; Page 279; 310pp; German.
XX
XX          This invention describes novel nucleic acid (cDNA) sequences (A) which
CC          have anticancer activity and are highly expressed in ovarian tumor
CC          tissue (and some also in testis and breast cancer tissue). The products
CC          of the invention can be used for gene therapy. (A) are used (i) for
CC          recombinant expression of polypeptides (B) and (ii) to isolate complete
CC          genes. (B) are used (i) to identify agents suitable for treatment of
CC          ovarian cancer; (ii) directly for treating this form of cancer
CC          (including expression from gene therapy vectors) and (iii) for generation
CC          of specific antibodies. (A) are identified by assembling ESTs (expressed
CC          sequence tags) from a particular tissue type before comparison of
CC          expression patterns. This allows a significantly longer fragment of the
CC          gene to be revealed, so should reduce the number of failures associated
CC          with the fact that ESTs from different libraries may represent different
CC          parts of the same unknown gene, distorting the estimated frequency of
CC          occurrence in a particular tissue. AY76505-Y76638 represent protein
CC          fragments encoded by the human ovarian tumor cDNA library derived EST
CC          fragments represented in AAZ77450-Z77372.
SQ
SQ          Sequence      194 AA;

Query Match              72.0%; Score 90; DB 20; Length 194;
Best Local Similarity    72.0%; Pred. No. 2, Le-05;
Matches   18; Conservative     2; Mismatches     3; Indels     2; Gaps     1.

QY          1 LDPMVKEOK--GKGPGAPPKDLMT 23
           II :III:I IIIIII III III
Db          106 LDALVKEKKIQKGGPGGPPLGLMY 130

RESULT 14
ABBS9646
ID          ABBS9646 standard; Protein; 1194 AA.
AC
XX          ABB59646;
AC
XX          26-MAR-2002 (first entry)
DT
DE          Drosophila melanogaster polypeptide SEQ ID NO 5730.
XX
XX          Drosophila; developmental biology; cell signalling; insecticide;
KW          pharmaceutical.
XX
XX          Drosophila melanogaster.
OS
PN          WO200171042-A2.
PN
XX          27-SEP-2001.
PD
XX          23-MAR-2001; 2001WO-US09231.
PF
XX          23-MAR-2000; 2000US-191637P.
PR
XX          11-JUL-2000; 2000US-0614150.
XX

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(PEKE) PE CORP NY.
 Venter JC, Adams M, Li PWD, Myers EW;
 WPI: 2001-656860/75.
 N-PSDB; ABL03749.
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 Disclosure: SEQ ID NO 5730; 21pp + Sequence Listing; English.
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA sequences (AB057737-AB072072) and the encoded proteins
 (AB057737-AB072072)
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 Sequence 1194 AA;

Query Match 43.2%; Score 54; DB 22; Length 1194;
 Best Local Similarity 64.3%; Pred. No. 29;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 5 VKOKGKPGGAPP 18
 : | | | | | | | | | |
 Db 613 MKSPNGNGPGAPP 626

RESULT 15

AAR79655
 ID AAR79655 standard; Protein; 298 AA.

AC AAR79655;

DT 06-DEC-1995 (first entry)

DE Human UBC/CDC34 protein.

KW Ubiquitin-conjugating enzyme; UBC/CDC34; cell cycle; cell proliferation; cancer; psoriasis; fibrosis.

OS Homo sapiens.

PN W09518974-A.

PD 13-JUL-1995.

PF 04-JAN-1995; 95WO-US00164.

PR 13-SEP-1994; 94US-0305520.

PR 04-JAN-1994; 94US-0176937.

PR 23-MAY-1994; 94US-0247904.

PR 27-MAY-1994; 94US-0250795.

PA (MITO-) MITOTIX INC.

PI Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;

DR WPI: 1995-255137/33.

DR N-PSDB; AAQ97845.

Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating e.g. cell proliferation

XX Disclosure; Page 107-108; 157pp; English.

XX Human UBC3/CDC34 cDNA (given in AAQ97845) was amplified from a HeLa cell cDNA library. The gene was subcloned into a baculovirus or pEX vector for expression of recombinant UBC/CDC34 in Sf9 insect or E. coli cells for use as a component of an in vitro ubiquitin conjugating system.

XX Sequence 298 AA;

Query Match 40.8%; Score 51; DB 16; Length 298;
 Best Local Similarity 61.5%; Pred. No. 19;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 KEOKGKPGGAPP 18
 : | | | | | | | | | |
 Db 21 EEAAGGPGGAPP 33

Search completed: April 11, 2003, 16:11:07
 Job time : 8.45351 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:33 ; Search time 36.6069 Seconds
(without alignments)
928.727 Million cell updates/sec

Title: US-09-821-726a-18_COPY_21_185

Perfect score: 880

Sequence: 1 DYSISVNDGNSGSGGQGV.....ISANIILNIFPCGIAEN 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	221.5	25.2	191	11	09D017	09d017 mus musculus
2	197	22.4	184	11	09C056	09c056 mus musculus
3	92	10.5	868	5	08S772	08s772 drosophila
4	86	9.8	285	5	094477	094477 dictyosteli
5	86	9.8	574	8	09M078	09m078 candida alb
6	83.5	9.5	186	5	001876	001876 caenorhabdi
7	83.5	9.5	1297	10	094556	094556 lycopersico
8	82.5	9.4	409	16	069974	069974 streptomyce
9	82.5	9.4	887	16	09J212	09j212 neisseria m
10	81	9.2	810	3	003388	003388 saccharomyc
11	81	9.2	1338	5	023927	023927 dictyosteli
12	80.5	9.1	263	10	048991	048991 oryza sativ
13	80.5	9.1	642	5	017169	017169 caenorhabdi
14	80	9.1	568	5	09N138	09n138 pinctada ma
15	79.5	9.0	227	10	P93572	P93572 solanum tub
16	79.5	9.0	526	10	Q9LJ56	Q9lj56 arabidopsis

17	79.5	9.0	855	5	08SV6	08sv6 dictyosteli
18	79	9.0	1060	5	08SS05	08ss05 dictyosteli
19	79	9.0	1318	5	095PH4	095ph4 dictyosteli
20	78.5	8.9	887	16	09J008	09j008 neisseria m
21	77	8.8	409	5	09BK6	09bk6 chaetopteru
22	77	8.8	409	5	09X2F6	09x2f6 chaetopteru
23	77	8.8	410	5	09W1W2	09w1w2 drosophila
24	77	8.8	808	16	09TE37	09te37 clostridium
25	77	8.8	1245	5	09G195	09g195 plasmodium
26	76.5	8.7	649	5	09VTX7	09vtx7 drosophila
27	76.5	8.7	764	5	09G234	09g234 plasmodium
28	76.5	8.7	1157	5	000895	000895 plasmodium
29	76.5	8.7	1298	5	09U010	09u010 plasmodium
30	76	8.6	573	4	094830	094830 homo sapien
31	76	8.6	588	5	0964F6	0964f6 plasmodium
32	75.5	8.6	241	2	033788	033788 salmonella
33	75.5	8.6	245	16	09ZRS8	09zrs8 rhizobium m
34	75.5	8.6	362	4	09UHS5	09uhs5 homo sapien
35	75.5	8.6	443	16	09PRE4	09pre4 staphylococ
36	75.5	8.6	608	17	08ZWK4	08zwk4 pyrobaculum
37	75.5	8.6	995	16	08Z086	08z086 salmonella
38	75	8.5	421	16	08YBP5	08ybp5 druceella me
39	75	8.5	434	5	08T834	08t834 dictyosteli
40	75	8.5	442	5	025830	025830 plasmodium
41	75	8.5	537	5	08T1K7	08t1k7 dictyosteli
42	75	8.5	4564	5	077075	077075 drosophila
43	74.5	8.5	1240	10	024016	024016 lycopersico
44	74.5	8.5	1266	10	09XET3	09xet3 lycopersico
45	74.5	8.5	1309	5	08T2H9	08t2h9 dictyosteli

ALIGNMENTS

RESULT 1
ID 09D017 PRELIMINARY: PRT: 191 AA.
AC 09D017;
DT 01-JUN-2001 (TREMBLrel, 17, Created)
DT 01-JUN-2001 (TREMBLrel, 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)
DE 1190003M12RIK Protein.
GN 1190003M12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=C57BL/6J; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitlaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004474; BAH23320.1; -;
DR MGD; MGI:1916138; 1190003M12RIK.

SEQUENCE 191 AA: 20772 MW: 76D7DB4796A8B4D CRC64:

Query Match 25.2%; Score 221.5; DB 11: Length 191;
 Best Local Similarity 31.2%; Pred. No. 8.6e-14;
 Matches 49; Conservative 31; Mismatches 60; Indels 17; Gaps 4;

13 GSSGGOVSVMNEHNVANNNGNNSMNAALMDYRTGFAVTRLFEEKSCIVHKKKEAMP 72
 42 GSVGTOTTHVDALRGVSTRDNSVQSEMDGMDYKNDLAAKLFKMACYLAKMDRAAPF 101
 73 SL-----QALDALVKEKKLOGKGPBG--PPPKSLRYSVNPNRVDNDLKFGRSIYAMCKGIP 126
 102 SLDDITGAL-----GKQASGHYPPTRGLTIVLPSRIKNAQYGVPIKDLGRAV 151

127 TYMA-ETIOGANLISYSEKISANILMILNISCSCGI 162
 152 TYFARQKKEGTALTPMDPSCSELQLLFMGLSIGEI 188

RESULT 2

ID 09CQ56 PRELIMINARY: PRT: 184 AA.

AC 09CQ56;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 1810036H07RIK protein.
 GN 1810036H07RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=STOMACH; AND PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Yamana K.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Fiedlschmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci F., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK006986; BAB26008.1;
 DR EMBL: AK007451; BAB25046.1;
 DR EMBL: AK007705; BAB25201.1;
 DR MGI:1913534; 1810036H07RIK.
 DR PRINTS: PR01559; DUFFYANTIGEN.
 SO SEQUENCE 184 AA: 20469 MW: 612A18FABE652230 CRC64;

Query Match 22.4%; Score 197; DB 11: Length 184;
 Best Local Similarity 29.4%; Pred. No. 2e-11;
 Matches 45; Conservative 37; Mismatches 67; Indels 4; Gaps 3;

12 SSGSGGOVSVMNEHNVANNNGNNSMNAALMDYRTGFAVTRLFEEKSCIVHKKKEAMP 71
 32 NGGTCGCTVITIDNOONTATINIHSGSCSTTIPYKKGITASRLSRACVITMDHKAT 91
 72 PSIALDALVKEKKLOGKGPBGPPKSLRYSVNPNRVDND--FKGSIVAMCKGIP 129

DB 92 PALDKLQRFLEKQTM-NAIDSPETWVRNPLKSLITKVDWELFGSPTRQLCKHMPLEY 150

QY 130 AEIOGANLISYSEKISANILMILNISCSCGI 162
 DB 151 GEVATRPKEVS-TGACAKYGLLGLGVSTICGCI 182

RESULT 3

ID 08SX72 PRELIMINARY: PRT: 868 AA.

AC 08SX72;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ID30050p.
 GN CG9381.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceoliker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY094811; AAM1164.1;
 SO SEQUENCE 868 AA: 92619 MW: E6FF05B4392EE3B CRC64;

Query Match 10.5%; Score 92; DB 5: Length 868;
 Best Local Similarity 23.8%; Pred. No. 2.5;
 Matches 30; Conservative 15; Mismatches 45; Indels 36; Gaps 3;

5 SYNDGNGSGGGOVSVMNEHNVANNNGNNSMNAALMDYRTGFAVTRLFEEKSCIVH 64
 86 NVNLINGSGNNNNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN 122

QY 65 KKKKEAMPSSLOALDALVKEKKLOGKGPBGPPKSLRYSVNPNRVDNDLKFGRKSIV-AMCK 123
 DB 123 --NKDANPNCHS-----GQGGGPNSPNGHNGRQNGNNGNNGNNGNNGNNGNTN 170

QY 124 GIPYIM 129
 DB 171 GPPDYM 176

RESULT 4

ID 094477 PRELIMINARY: PRT: 285 AA.

AC 094477;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ORFveg158 (Fragment).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Loomis W.F.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U66524; AAB06787.1;
 DR InterPro: IP001849; PH.
 DR Pfam: PF00169; PH; 1.
 DR SMART: SM00233; PH; 1.
 FT NON_TER 1
 SO SEQUENCE 285 AA: 31010 MW: A1AF742F99AAE36 CRC64;

34 NNGWNSWNL-----WDRTGFAVTRLFEEKSCIVHIKKKEAMP-----SLQALDALVKE 83

DB 293 NENYENMNDLRNIFVODIGSKITVT---TRKDSVALMNGNEOISMGNLSTASWSLFFKR 349

OY 84 KLIQGGPGGPPPKSLRYSVNPNKRVNDLDFKGSIVAMCKGIPTVMAEEIOGANLISYE 143

DB 350 HAFENMDPMKHP-----ELEBYGROIACKGGLP--LAKTLAGLRLRKSE 393

OY 144 ----KCSIANILMIL 154

DB 394 IDEMKCLIRSEIMEL 408

RESULT 8

069974 PRELIMINARY; PRT; 409 AA.

AC 069974: 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

GN Putative secreted protein.

OS SC05798 OR SC4H2.19C.

OC Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RA SEQUENCE FROM N.A.

RC STRAIN-A3(2) / M145;

RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,

RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Raddlowski E., Rajandream M.A., Rutherford K., Ruter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2)";

RL Nature 417:141-147(2002).

DR EMBL; AL022268; CAA18335.1. -

SQ SEQUENCE 409 AA; 42955 MW; F99AEF3D5FE14E5B CRC64;

Query Match 9.4%; Score 82.5; DB 16; Length 409;

Best Local Similarity 21.1%; Pred. No. 8.3;

Matches 39; Conservative 21; Mismatches 74; Indels 51; Gaps 7;

OY 3 SISVNDGSGGSGQSVSVNHNHNAVNDN--NNGMNSMN-----AL 43

DB 54 SASAADGNGGIRIPDDIKDLKEHGDIDVDMKNGAMKMKMNDMLREAOFPVPIIEGL 113

OY 44 WDRYGFATVRLFEKSCIVHMKMKKEAMPISLALDALVREKKLOG-KGPGPPKSLRYS 102

DB 114 WD-----PRMRDAEPPDQEVENDISGOGVTPDPAPVAE 151

OY 103 VNPENRV-DNLDFKGSIVAMCKGIPTVMAEEIOG-----ANLISSEKISANIL--WI 153

DB 152 AVPAKYHDMNAATGAKLLDFSPKSGMVCATVYKDPAPKPSNMVWTAAGCHVAGKSGGWY 211

OY 154 LNISE 158

DB 212 RNIAF 216

RESULT 9

09J212 PRELIMINARY; PRT; 887 AA.

AC 09J212: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

GN Pyruvate dehydrogenase, E1 component.

OC Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=491;

RN [1]

RA SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;

RX MEDLINE=20175755; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Nelson W.C., Gwyn M.L., Deboy R., Peterson J.D., Hickey E.K.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Citron E.B.,

RA Cotton M.D., Ullrich T.R., Kouri H., Qin H., Yamahara J.,

RA Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;

RA "Complete genome sequence of Neisseria meningitidis serogroup B strain

RT MC58";

RL Science 287:1809-1815(2000).

DR EMBL; AE002462; AAF41716.1. -

DR TIGR; NMB1341; -

DR InterPro; IPR004660; ACEE.

DR InterPro; IPR000360; Transketolase.

DR Pfam; PF00456; Transketolase; 1.

DR TIGRFAMS; TIGR00759; acee; 1.

RW Complete proteome.

SQ SEQUENCE 887 AA; 99562 MW; BA7BA93E38C5206F CRC64;

Query Match 9.4%; Score 82.5; DB 16; Length 887;

Best Local Similarity 24.1%; Pred. No. 21;

Matches 41; Conservative 24; Mismatches 60; Indels 45; Gaps 9;

OY 9 DGNSSGSGGQSVSVNHNHNAVNDNNGN-----SMNALMDYRTGFATVRLFEK-KSCIV 63

DB 264 DDPVGNCK--IIQELGNFAGA-----GNVYKVIWGRMD-----RLAKKDKDIL 309

OY 64 HKMKKAM-----PSLQALDALVREKKLOG-KGPGPPKSLRY 101

DB 310 RQRMEECLDGDYQYTKSKKGDYVREHFNTPELKALVADMTDEQJMALRNGCHDPOKY-Y 368

OY 102 SVNPNRVNDLDFKGSIVAMCKGIPTV-MAEEIOGANLISSEKISANI 150

DB 369 NAYDRANHAD--GKPTVILARTITKGYGMSGSGEONVAHOKMKDKASL 416

RESULT 10

003388 PRELIMINARY; PRT; 810 AA.

AC 003388: 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

GN YDR485C OR D8035.28.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RA SEQUENCE FROM N.A.

RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,

RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,

RA Hunkle-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,

RA Mosegale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,

RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,

RA Winant A., Yelton M., Botstein D., Davis R.W.;

RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

RL [2]

RN [2]

RA SEQUENCE FROM N.A.

RA Dietrich F.S.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RA SEQUENCE FROM N.A.

RA Jia Y., Cherry J.M.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: U33050; AAB64928.1; -
 DR SCD; S0002893; YDR485C.
 SQ SEQUENCE 810 AA; 92247 MW; D49FECADD9C0093 CRC64;

Query Match
 Best Local Similarity 23.6%; Score 81; DB 3; Length 810;
 Matches 26; Conservative 25; Mismatches 39; Indels 20; Gaps 5;

OY 5 SVNDGSGSGGSOVSNNHHVANNVNNNN---GNMSNMLMDYRTGFAVTRLEKKS 61
 DB 364 SIKNDGDVNSLGENSSSVHOKRIETSTNDYVEGESSPA-----ASRVNS---- 411
 OY 62 IVHKKMKKEMPQLDALVKEKKLGKGGPPPKSLRYSVNPVRNDL 111
 DB 412 --DELKPTALPDV-TLDAIANKOSTVDEAPNSQPKNI--ITTEOKITNV 456

RESULT 11

O23927 PRELIMINARY; PRT: 1338 AA.
 AC O23927;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Protein tyrosine kinase.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX-2;
 RA Adler Kristin.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U64830; AAB04999.1; -
 DR HSP; P08631; IAD5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR001245; TYR_pkinase.
 DR Pfam: PF00069; pkinase; 2.
 DR ProDom: PD000001; Euk_pkinase; 2.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; kinase; transferase; tyrosine-protein kinase.
 SQ SEQUENCE 1338 AA; 149926 MW; D257958DD717C02 CRC64;

Query Match
 Best Local Similarity 22.7%; Score 81; DB 5; Length 1338;
 Matches 42; Conservative 23; Mismatches 42; Indels 78; Gaps 8;

OY 7 NDDGNSG-----GSGQGSVSNNHHVANNVNNNNGNMNLMDYRTG 50
 DB 465 NNINNSGIRRSADDTVTLSPTLSSGSSSTSSNPHN-PNHHQKLN----- 512
 OY 51 AVTRLEKKSCTIVHKKMKKEMPQLDALVKEKKLGKGGPPPKSLRYSVNPVRND 110
 DB 513 ---KLEKLSCT---TRKEITELLEKKSLEKONLIDEG-----YSENADSPEN 555
 OY 111 LDKRGKSVAMCKGIPYIMAEIQANLISYEKCI-----SANTILITLISRCG 160
 DB 556 L-----SFEIOLKIN-----EKIIELENLITSLSNSNWSLNGSSSTS 592
 OY 161 GIAEN 165
 DB 593 TISCN 597

RESULT 12

ID O48991 PRELIMINARY; PRT: 263 AA.
 AC O48991;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE NBS-LRR type resistance protein (Fragment).
 GN R11.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE.
 RX MEDLINE=98081880; PubMed=9419382;
 RA Leister D., Kurth J., Laurie D.A., Yano M., Sasaki T., Devos K.,
 RT "Rapid reorganization of resistance gene homologues in cereal
 genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:370-375(1998).
 DR EMBL: AF032698; AAB96995.1; -
 DR InterPro: IPR000767; Disease-resist.
 DR InterPro: IPR002182; NB-ARC.
 DR Pfam: PF00931; NB-ARC; 1.
 DR PRINTS: PR00364; DISEASERESIST.
 FT NON_TER 1 1
 FT NON_TER 263 263
 SQ SEQUENCE 263 AA; 30261 MW; 476A54B153B105BC CRC64;

Query Match
 Best Local Similarity 21.7%; Score 80.5; DB 10; Length 263;
 Matches 26; Conservative 25; Mismatches 50; Indels 19; Gaps 4;

OY 15 SGQGSVSNNHHVANNVNNNNGNMNLMDYRTGFAVTRLEKKSCTIV-----HKMK 68
 DB 59 SPHERLAKRIKHKVLLVLDLNNRRCMD-----LICEPMNTALCMITYTRSERVAK 114
 OY 69 --EAMPQLDALVKEKKLGKGGPPPKSLRYSVNPVRNDLDRGKSVAMCKGIP 126
 DB 115 LVOTMPNPTSLNCLSSSEWS-----LKKQVAFVYDNGMTPNLQELGMSIVKCKGLP 167

RESULT 13

ID O17169 PRELIMINARY; PRT: 642 AA.
 AC O17169;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 68.1 kDa protein.
 GN B0454.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Geisel C., Beck C., Gibson A.;
 RT "The sequence of C. elegans cosmid B0454.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.


```

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CAIL protein homolog.
GN CAIL.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Welt C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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CC -----
DR EMBL: AK008990; BAB26010.1; -
DR EMBL: AK008622; BAB25784.1; -
DR EMBL: AK008641; BAB25801.1; -
DR EMBL: AK008647; BAB25805.1; -
DR EMBL: AK008722; BAB25856.1; -
DR EMBL: AK008745; BAB25872.1; -
DR EMBL: AK008933; BAB25875.1; -
DR EMBL: AK008956; BAB25988.1; -
DR EMBL: AK009145; BAB26103.1; -
DR EMBL: AK019050; BAB31525.1; -
DR MGI: MGI:1913533; 2200002K21R1K.
FT CONFLICT 113 113 P -> L (TN REF. 1; BAB26103).
SQ SEQUENCE 184 AA; 20134 MW; 2889820404FF8B CRC64;
Query Match 67.4%; Score 593.5; DB 1; Length 184;
Best Local Similarity 65.9%; Pred. No. 7.2e-50;
Matches 108; Conservative 22; Mismatches 31; Indels 3; Gaps 2;
OY 2 YSISVN-DGNGSGGSGQSVNNEHNVANVDNNNGNSMNLMDYRTGFAVTRLEFKS 60
DB 21 YVNIINGNDGNDVSGQSVSINGVNHVANNIDNNNGMSNIMDXYENFATRLFSKKS 80
OY 61 CIVRRKKRKAAMPSTQALDALVKEKKLOGGPGPKSLRYSVNPRVRNDLDFGSGSYA 120
DB 81 CIVHRMNDAMPSTQDLDTMVEKK--GKPGGAPPKDLIMYSVNPFRVLDLTFGPKTAG 138
OY 121 MCKGIPYMAETIGCANLISSEKCSANIILMIILNISFGCGIAE 164
DB 139 MCRGIPYVAEETPGPNQPLVSKKCYTADILMLRMSFGTSVE 182

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RESULT 3
ID NRPI_YEAST STANDARD; PRT; 719 AA.
AC P32770; Q12228;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Asparagine-rich protein (ARP protein).
DE NRPI OR ARP1 OR ARP OR YDL167C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=AH22;
RX MEDLINE=93247548; PubMed=8483449;
RA Wehner E.P., Rao E., Brendel M.;
RT "Molecular structure and genetic regulation of SFA, a gene
RT responsible for resistance to formaldehyde in Saccharomyces
RT cerevisiae, and characterization of its protein product.";
RL Mol. Gen. Genet. 237:351-358(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Polh T.M.;
RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
CC -----
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CC -----
DR EMBL: X68020; CAA48159.1; -
DR EMBL: Z67750; CAA91579.1; -
DR EMBL: Z74215; CAA98741.1; -
DR PTR: S31139; S31139.
DR SGD: S0002326; NRPI.
DR InterPro: IPR000504; RNA_rec-mot.
DR InterPro: IPR001876; Znf-RanGDP.
DR Pfam: PF00076; rrm; 1.
DR Pfam: PF00641; zf-RanBP; 2.
DR SMART: SM00360; RRM; 1.
DR SMART: SM00547; ZNF_RBP2; 2.
DR PROSITE: PS0102; RRM_1; FALSE_NEG.
DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
DR PROSITE: PS01358; ZF_RANBP2_1; 2.
DR PROSITE: PS0199; ZF_RANBP2_2; 2.
KW Nuclear protein; Zinc-finger; RNA-binding; Repeat.
FT DOMAIN 226 322
FT ZN_FING 355 384
FT ZN_FING 581 610
FT ZN_FING 564 564
FT DOMAIN 490 490 RANBP2-TYPE 1.
FT CONFLICT 493 493 ASN-RICH.
FT CONFLICT 493 493 I -> N (TN REF. 1)
SQ SEQUENCE 719 AA; 79299 MW; ADA9BC09F58269 CRC64;
Query Match 10.7%; Score 94.5; DB 1; Length 719;
Best Local Similarity 24.8%; Pred. No. 0.25;
Matches 39; Conservative 18; Mismatches 63; Indels 37; Gaps 5;
OY 2 YSISVNDGNSGSGQSVNNEHN-----VANVDNNNGNSMNLMD 44
DB 508 YVNIINGNDGNDVSGQSVSINGVNHVANNIDNNNGMSNIMDXYENFATRLFSKKS 567
OY 45 DYRTGFAVTRL-----FEKSCIVHKRKKKAM-----PSLDALDALVKEKKLOGK--G 90
DB 568 NIGMGCGSGNMFRAGDMKSTCTYHNFAKNVYCLRCGGPKSISGDSATNHYIDSTFG 627

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OY 91 PGPPPKSLRYSVNPN-----RVNDLDFGKSIYAM 121
 Db 628 PASRTFNNNNISVNTNGSGNACRTGNDNKKGRDISLM 664

RESULT 4

ID DVL1_MOUSE STANDARD: PRT: 695 AA.

AC P51141: 060868; (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
 DE (DSH homolog 1).
 GN DVL1 OR DVL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=95046919; PubMed=7958461;
 RA Sussman D.J., Klingensmith J., Salinas P., Adams P.S., Nusse R.,
 RA Perrimon N.;
 RT "Isolation and characterization of a mouse homolog of the Drosophila
 RT segment polarity gene dishevelled.";
 RL Dev. Biol. 166:73-86(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=96632916; PubMed=9132266;
 RA Lijam N., Sussman D.J.;
 RT "Organization and promoter analysis of the mouse dishevelled-1 gene.";
 RL Genome Res. 5:116-124(1995).
 RN [3]
 RP KNOCK-OUT.
 RX MEDLINE=97442352; PubMed=9298901;
 RA Lijam N., Paylor R., McDonald M.P., Crawley J.N., Deng C.-X.,
 RA Herrup K., Stevens K.E., Maccaferri G., McBain C.J., Sussman D.J.,
 RA Wyszynski B.;
 RT "Social interaction and sensorimotor gating abnormalities in mice
 RT lacking Dvl1.";
 RL Cell 90:895-905(1997).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES. DVL1 DEFICIENT MICE DISPLAY
 CC ABNORMALITIES IN SOCIAL BEHAVIORS AND SENSORIMOTOR GATING.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE BRAIN, TESTIS AND
 CC KIDNEY. LOWER LEVELS IN THE OVARY, BREAST, MUSCLE, LIVER AND SMALL
 CC INTESTINE. AND VERY LOW LEVELS ARE SEEN IN THE SPLEEN AND THYMUS.
 CC A MODERATE LEVEL EXPRESSION IS SEEN IN THE HEART.
 CC DEVELOPMENTAL STAGE: IS EXPRESSED THROUGHOUT THE EMBRYONIC CENTRAL
 CC NERVOUS SYSTEM FROM PRESOMITE STAGES AND IN NEURON-RICH AREAS OF
 CC THE BRAIN THROUGHOUT POSTNATAL DEVELOPMENT, AS WELL AS IN MANY
 CC OTHER TISSUES.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -----
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 CC -----
 CC EMBL: 010115; AAA82175.1;
 CC EMBL: 028138; AAA74049.1;
 CC HSSP: 012923; 3PDZ.
 CC MGD: MGI:94941; DVL.
 CC InterPro: IPR000591; DEP.

DR InterPro: IPR001158; DIX.
 DR InterPro: IPR003351; Dishevelled.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ; 1.
 DR Pfam: PF00610; DEP; 1.
 DR Pfam: PF00778; DIX; 1.
 DR Pfam: PF02377; Dishevelled; 1.
 DR Prodom: PD003639; DIX; 1.
 DR SMART: SM00021; DAX; 1.
 DR SMART: SM00049; DEP; 1.
 DR SMART: SM00228; PDZ; 1.
 DR PROSITE: PS50186; DEP; 1.
 DR PROSITE: PS50106; PDZ; 1.
 KW Developmental protein.
 FT DOMAIN 251 323 PDZ.
 FT DOMAIN 425 489 DEP.
 FT DOMAIN 390 393 POLY-SER.
 FT CONFLICT 122 125 MISSING (IN REF. 2).
 FT CONFLICT 211 211 T -> N (IN REF. 2).
 SQ SEQUENCE 695 AA; 75350 MW; A9FA449F5C75F2 CRC64;

Query Match 9.9%; Score 87; DB 1; Length 695;
 Best Local Similarity 26.8%; Pred. No. 1.2;
 Matches 30; Conservative 15; Mismatches 49; Indels 18; Gaps 5;

OY 12 SGSGGGSVSVNNEHNVANDNNNGNSMALDYRTGFAVTRLEFKKSCIVHKKKEAM 71
 Db 596 AGSGSGSES-----DHTVPSGSGSTGW-----WER-----FVSQLSKSS--PSSQASAVA 638
 OY 72 PSLQALDAIVKERRKIOGKGGPPPKSLRYSVNPNRVNDLDFGKSIYAMCK 123
 Db 639 GGLPLPLPLTKAVAVVGGPPGPPVRELA-AVPELITGSPQSKAMGNCE 689

RESULT 5

ID DVL1_RAT STANDARD: PRT: 695 AA.

AC Q9WB99; Q9WB98; Q9W0C5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
 DE (DSH homolog 1).
 GN DVL1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar Kyoto;
 RX MEDLINE=21254118; PubMed=11354832;
 RA de Lange R.P.J., Burr K., Clark J.S., Negrin C.D., Brosnan M.J.,
 RA St Clair D.M., Domanczak A.F., Shaw D.J.;
 RT "Mapping and sequencing rat dishevelled-1: a candidate gene for
 RT cerebral ischemic insult in a rat model of stroke.";
 RL Neurogenetics 3:99-106(2001).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN
 CC -----
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 CC -----
 CC EMBL: AF143545; AAD33896.2; -.

DR EMBL: AF143546; AAC33897.2; -
 DR EMBL: AF143548; AAD41492.2; -
 DR EMBL: AF143547; AAD41492.2; JOINED.
 DR EMBL: AF143550; AAD41493.1; -
 DR EMBL: AF143549; AAD41493.1; JOINED.
 DR InterPro: IPR000591; DEP.
 DR InterPro: IPR001158; DIX.
 DR InterPro: IPR003351; Dishevelled.
 DR InterPro: IPR001478; PDZ.
 DR Pfam: PF00595; PDZ.1.
 DR Pfam: PF00610; DEP.1.
 DR Pfam: PF00778; DIX.1.
 DR Pfam: PF02377; Dishevelled.1.
 DR ProDom: PD003639; DIX.1.
 DR SMART: SM00021; DAX.1.
 DR SMART: SM00049; DEP.1.
 DR PROSITE: PS00186; DEP.1.
 DR PROSITE: PS0106; PDZ; PARTIAL.
 KW Developmental protein.
 FT DOMAIN 251 323 PDZ.
 FT DOMAIN 425 499 DEP.
 SQ SEQUENCE 695 AA; 75447 MW; EEC4AA99A117D22A CRC64;

Query Match 9.9%; Score 87; DB 1; Length 695;
 Best Local Similarity 26.8%; Pred. No. 1.2;
 Matches 30; Conservative 15; Mismatches 49; Indels 18; Gaps 5;

QY 12 SGSSGQSVNNEHNVANDNNNGNSWALMDYRTGFAVTRLEFKKSCIVHKKKEAM 71
 DB 596 AGGSSSES-----DHYPSGSSGSGTW-----WER-----PVSQLSRGS--PRSCASAVA 638
 QY 72 PSIALDALVKEKKLOGKPGGPGPKSLRYSVNNRVNDLDFGKSIVAMCK 123
 DB 639 PGLPPLPLTKAVAVVGGPGGPPVRELA-AVPELTLGSRGSPQKAMGNPCE 689

RESULT 6
 DPSD_CLOPA STANDARD; PRT; 296 AA.

AC 046192;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 6013;
 RA Meyer J.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Phosphatidyl-L-serine -
 phosphatidylethanolamine + CO(2).
 CC -1- CORRECTOR: Pyruvoyl group (by similarity).
 CC -1- PATHWAY: Aminophospholipid biosynthesis.
 CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST PSD2.
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DR EMBL: Z28353; CAAB2212.1; -
 DR InterPro: IPR003817; PS_Decarboxylase.
 DR InterPro: IPR005221; PS_Decarb.
 DR Pfam: PF02666; PS_Decarboxylase.1.
 DR TIGRFAMS: TIGR00163; PS_Decarb.1.
 KW Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.

FT SITE 255 256 CLEAVAGE (NONHYDOLYTIC)
 FT (BY SIMILARITY).
 FT MOD_RES 256 256 CONVERTED TO A PYRUVYL GROUP
 FT (BY SIMILARITY).
 SQ SEQUENCE 296 AA; 34243 MW; A131FA6D2F80472A CRC64;

Query Match 9.4%; Score 83; DB 1; Length 296;
 Best Local Similarity 27.3%; Pred. No. 1;
 Matches 36; Conservative 18; Mismatches 46; Indels 32; Gaps 6;

QY 20 VSVNNEHNVANDNNNGNSWALMDYRTGFAVTRLEFKKSCIVHKKKEAMPSQLALDA 79
 DB 116 IIVYNNIMNMNIIQVKGIT--YKLNLDLQNDISIKVEKGTCLIALCPDYHFRHFLDN 173
 QY 80 LVKEKKLOGKPGGPGPKSLRYSVNP-----NRVDL-----DKFGK-----SIV 119
 DB 174 GICESTIKITGN-----YYSVNPALINKINLNFCKRMKREMSFNSDNGKILYVEIG 225
 QY 120 AMCKG--IPTYM 129
 DB 226 ATCVSGSIQTYM 237

RESULT 7
 TL29_ARATH STANDARD; PRT; 349 AA.

ID TL29_ARATH
 AC P82281; Q9M0S6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Putative L-ascorbate peroxidase, chloroplast precursor (EC 1.11.1.11)
 DE (Thylakoid lumenal 29 kDa protein) (TL29) (P29).
 GN ARAF09010 OR F23J3.40.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv Columbia;
 RA MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schnell R., Murphy G., Volkert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Ertian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Griwell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Oberwaller B., Macho R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnsels J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Welzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Beutelsma P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernstier S., Hempel S., Feldpausch M., Lambert H., Van den Daele H.,
 RA de Keyser A., Buysaert C., Gielen J., Villalroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail R., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K.,
 RA Pettelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Botkova D., Bloeker H., Scharte M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Farman B., Graeberth K., Dauner D., Herzl A.,
 RA Neumann S., Argilou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Ougliero F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedror F., Cooke R., Berger C., Montfort A., Casachuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bietle C.,
 RA Frishman D., Haase D., Lemcke K., Meves H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,

```

OS Bacillus thuringiensis.
CC Bacteria:Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN 111
SEQUENCE FROM N.A.
STRAIN=NRRL B-18246 / P563B:
RA Schneck H.E., Schwab G.E., Payne J.M., Narva K.E., Foncecrada L.;
RT "Novel nematode-active toxins and genes which code therefor.";
RL Patent number W09219739, 09-DEC-1992.
CC -1- FUNCTION: ENDOTOXIN WITH NEMATOCIDAL ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPOROGATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -1- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
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CC -----
CC EMBL: L07023; AAA22356.1; -.
CC InterPro: IPR001178; Endotoxin.
CC Pfam: PF00555; endotoxin; 1.
CC Toxin: Sporulation.
CC KW TOXIN; Sporulation.
CC SQ SEQUENCE 803 AA; 88142 MW; 680E57C6A246A826 CRC64;
Query Match 8.8%; Score 77; DB 1; Length 803;
Best local Similarity 25.5%; Pred. No. 13;
Matches 41; Conservative 19; Mismatches 73; Indels 28; Gaps 9;
QY 7 NDDGNSGC---SCQASVSNNHHNVN-VDNNGGMSMWNLW-DYRTGFAYTLEFKKSC 61
DQ 420 NDPGLSGDVLPAPMSV-VNAQTOTQAYDGENIMWIDTGRSMVLCTLRGCTTCFPGRC 478
QY 62 IVH-----KMKKEAMP--SLQALDALVKEKKLOGKRGHGPSPSLYSVAPNR-VNLLRK 113
DB 479 YNNSGCGESCNSGLPGOKIHATLPYQTVNLQSGGLGLASHIPYDLSFNNITIGDKD 528
QY 114 FKSIVAMCKGIPF-----YMAERIOGANLISYS 142
DB 539 DSTNIVA--KGIPIVEKGYASSGQVVEILREMINCANVQOLS 577
RESULF 9
XNNA_RUMFL STANDARD: PRT: 954 AA.
ID_XNNA_RUMFL
AC P29126;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase xyla precursor (EC 3.2.1.8).
GN XNNA.
OS Ruminococcus flavefaciens.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;
OC Ruminococcus.
OX NCBI_TaxID=1265;
RN 11
SEQUENCE FROM N.A.
RA STRAIN=17;
RA MEDLINE=92261318; PubMed=1584021;
RA Zhang J.-X., Flint H.J.;
RT "A bifunctional xylanase encoded by the xyna gene of the rumen
RT cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
RT dissimilar domains linked by an asparagine/glutamine-rich sequence."
RT Mol. Microbiol. 6:1013-1023(1992).
CC -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYL0-OLIGOSACCHARIDES
CC AND DOMAIN 2 MORE XYLOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

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CC      linkages in xylans.
CC      -1- PATHWAY: Xylan degradation.
CC      -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC      G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC      -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC      F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----

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DR	EMBL: Z11127: CAA77476.1; -	
DR	PIR: S18043: S18043.	
DR	PIR: S20907: S20907.	
DR	HSSP: P48793; 1XND.	
DR	InterPro: IPR001137; GH_11.	
DR	InterPro: IPR001000; Glyco_hydro.10.	
DR	Pfam: PF00331; Glyco_hydro.10; 1.	
DR	Pfam: PF00457; Glyco_hydro.11; 1.	
DR	PRINTS: PR00134; GLHYDRASE10.	
DR	PRINTS: PR00911; GLHYDRASE11.	
DR	PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.	
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11; 1.	
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F12; 1.	
KW	Xylan degradation; Hydrolase; Glycosylase; Multifunctional enzyme;	
KW	Repeat; signal.	
FT	SIGNAL	1
FT	CHAIN	27
FT	DOMAIN	28
FT	DOMAIN	28
FT	DOMAIN	245
FT	DOMAIN	623
FT	ACT_SITE	122
FT	ACT_SITE	122
FT	ACT_SITE	223
FT	ACT_SITE	774
FT	ACT_SITE	884
SEQUENCE	954 AA; 11362 MW; 1033567DAB526EBD CXC64;	
	OR 28, OR 29 (POTENTIAL).	
	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA.	
	XYLANASE DOMAIN 1.	
	ASN/GLN/TRP-RICH (LINKER).	
	XYLANASE DOMAIN 2.	
	NUCLEOPHILE (BY SIMILARITY).	
	PROTON DONOR (BY SIMILARITY).	
	PROTON DONOR (BY SIMILARITY).	
	NUCLEOPHILE (BY SIMILARITY).	

	Query Match	8.8%	Score 77	DB 1	Length 954
Best Local Similarity	39.1%	Pred No. 17			
Matches 18; Conservative	6;	Mismatches 18;	Indels 4;	Gaps 2	
OY	3	SISVYDGGNSGGGSOOSVSVNNEHHVANDNNNNNSW--	NALMD	45	
	1:1	1:1	1:1	1:1	1:1
Db	235	SISVYGGGSSDNGGGOQNNNDMDQD-N	NNQDQNNNDNNMGQNNNDNN	279	

ID	TL29_LYCES	STANDARD:	PRT:	345 AA.
AC	09THX6;			
DT	16-OCT--2001 (Rel. 40, Created)			
DT	16-OCT--2001 (Rel. 40, Last sequence update)			
DT	16-OCT--2001 (Rel. 40, Last annotation update)			
DE	Putative L-ascorbate peroxidase, chloroplast precursor (EC 1.11.1.11)			
DE	(Thylakoid lumenal 29 kDa protein) (TL29) (P29).			
GN	CLHB339.			
OS	Lycopersicon esculentum (tomato).			
OC	Euxariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Assteridae; easterids I; Solanales; Solanales; Solanales; Solanum.			
OX	NCBI_TaxID=4081;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.			
RA	MEDLINE=20487156; PubMed=11034343;			
RA	Kieselbach T., Bystrød M., Hynds P., Robinson C., Schroeder W.P.;			
RT	"A peroxidase homologue and novel plastocyanin located by proteomics			
RT	for the Arabidopsis thylakoplast thylakoid lumen.",			
FEBS Lett.	480:271-276 (2000).			
CC	-!- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN			

CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) = dehydroascorbate + 2
CC H(2)O.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC -1- SIMILARITY: TO ASCORBATE PEROXIDASES.
CC -----
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DR	EMBL: A251882; CAB64343.1; -	
DR	HSSP: P46534; IAPX	
DR	InterPro: IPR002016; Peroxidase.	
DR	Pfam: PF00141; Peroxidase; 1.	
KW	Oxidoreductase; Peroxidase; Hydrogen peroxide; chloroplast;	
KW	Transit peptide; Thylakoid.	
FT	TRANSIT 1 ?	CHLOROPLAST (POTENTIAL).
FT	TRANSIT ? 78	THYLAKOID (BY SIMILARITY).
FT	CHAIN 79 345	PURATIVE L-ASCORBATE PEROXIDASE.
SO	SEQUENCE 345 AA; 37749 MW; 681CAEBFDDBB41B CRC64;	

Query Match	8.6%;	Score 76;	DB 1;	Length 345;
Best Local Similarity	28.6%;	Pred. No. 5.9;		
Matches	32;	Conservative	16;	Mismatches 43.

[illegible]

ID	RLR1_YEAST	STANDARD:	PRT:	1597 AA.
AC	P53552;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	RLR1 protein (THO2 protein) .			
GN	RLR1 OR THO2 OR YNL139C OR NL209 OR NL835.			
OS	Saccharomyces cerevisiae (Baker's Yeast) .			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			

RP SEQUENCE FROM N.A.
RC STRAIN-IM256:
RA West R.W., Kruger B., Thomas S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C:
RX MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Busseureau F., Jaquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MEA2,
MEP2, CAP/SRY2, NAA9, FKb1/FPRI/RBP1, MOM22 and Cpl1, predicts an
adenosine deaminase gene and 14 new open reading frames.";
RL J. Eukaryot. Microbiol. 42:1195-1209(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98372750; PubMed=9707445;
RA Pirnat J.I., Aguilera A.;
RT "A novel yeast gene, THO2, is involved in RNA pol II transcription and
provides new evidence for transcriptional elongation-associated
recombination.";
RL EMBO J. 17:4859-4872(1998).

CC -1- FUNCTION: PILOTROPIC REGULATORY PROTEIN INVOLVED IN POST-
 CC TRANSCRIPTION INITIATION CONTROL. INVOLVED IN RNA POLYMERASE II
 CC TRANSCRIPTION.
 CC -1- SIMILARITY: TO S.POMBE SPAC22F3.14C.
 CC -----
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 CC -----
 CC EMBL: U22361; AAA93160.1; -
 CC DR EMBL: Z46843; CAA86886.1; -
 CC DR EMBL: Z71416; CAA96023.1; -
 CC DR SGD: S0005083; RLRI.
 CC KW Transcription regulation.
 CC SEQUENCE 1597 AA; 183930 MW; 5F1993C3726F298 CRC64;
 SQ
 Query Match 8.6%; Score 76; DB 1; Length 1597;
 Best Local Similarity 22.6%; Pred. No. 39;
 Matches 43; Conservative 32; Mismatches 61; Indels 54; Gaps 10;
 OY 28 VANVDNNGNSWNL--W-DY--RTGFAVTRL-----FEKKSCT 62
 DB 554 VADIQNHGSESLHTIDKIDYRKFIPTATSLONNPATSEVYELMKFPPEKRYFI 613
 OY 63 VHKM-----KKEAMPISQAL--DALVKEKKLGCKPGCPKPSLRYS 102
 DB 614 YNEWMKRLSODILPLKVSFKAREKSLTKALSIDTIKESRPAKLISTNLASLIVA 673
 OY 103 VNPBRVNLKFGKSIYAMCKGIPTVMAEIEGANTL--ISYSEKGISAN---TLWILNI 156
 DB 674 V--KQINRYKVSLEYVTTTKRYNDFAVDLQFVLLRLTYNRPAAVDFDGNQAMWVQL 721
 OY 157 S-FCGGAEN 165
 DB 732 SIFAGLAKN 741
 RESULT 12
 CSP_PLAFW STANDARD: PRT: 442 AA.
 ID CSP_PLAFW STANDARD: PRT: 442 AA.
 AC P08307;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Circumsporozoite protein precursor (CS).
 OS Plasmodium falciparum (isolate Welmcome).
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5848;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lockyer M.J., Schwartz R.T.; PubMed=3543671;
 RT "Strain variation in the circumsporozoite protein gene of Plasmodium
 RT falciparum.";
 RT Mol. Biochem. Parasitol. 22:101-108(1987).
 CC -1- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
 CC SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
 CC MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
 CC VERTEBRATE HOST). THE C-TERMINAL REGION IS PROBABLY USED FOR
 CC ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES
 CC WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
 CC -1- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
 CC -----
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 CC -----
 CC EMBL: M15505; AAA29554.1; -
 CC DR PIR: A54529; A54529.
 CC DR InterPro: IPR003067; Circumsporozoite.
 CC DR InterPro: IPR000884; TSP1.
 CC DR Pfam: PF00090; TSP1.1; 1.
 CC DR PRINTS: PR01303; CIRCUMSPOROITE.
 CC DR SMART: SM00209; TSP1; 1.
 CC KW Malaria; Sporozoite; Repeat; Signal.
 CC FT SIGNAL 1 16
 CC FT CHAIN 17 442 CIRCUMSPOROZOITE PROTEIN.
 CC FT DOMAIN 130 320 47 X 4 AA tandem repeats of N-A-N-P.
 CC SEQUENCE 442 AA; 47402 MW; BD579A152B85E03 CRC64;
 SQ
 Query Match 8.5%; Score 75; DB 1; Length 442;
 Best Local Similarity 28.2%; Pred. No. 10;
 Matches 31; Conservative 13; Mismatches 34; Indels 32; Gaps 5;
 OY 3 SISVNDGNSGSGGQSVSNNEHNVAVDNNNGNSWNLMDYRTGFAVTRLFEKKSCT 62
 DB 71 SLGNDDD-----NDGNNNNNGNNNDNG-----REG-----KDDKRDGN 108
 OY 63 VHKMKEAMPISQALDALVKEKKLGCKPGCPKPSLRYSNPBRVNL 112
 DB 109 NEDNKKLRP-----KHKTKQPGDGNPDPA-NPNDVPA NPNDV 148
 RESULT 13
 KCOL_ARATH STANDARD: PRT: 728 AA.
 ID KCOL_ARATH STANDARD: PRT: 728 AA.
 AC Q39017; Q9SD92;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Diacylglycerol kinase I (EC 2.7.1.107) (Diglyceride kinase 1)
 DE (DGK 1) (DAG kinase 1).
 GN DGK1 OR AT5G07920 OR F13G24.120 OR MXM12.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Columbia;
 RC MEDLINE=96189276; PubMed=8605313;
 RX Katagiri T., Mizoguchi T., Shinozaki K.;
 RT "Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in
 RT Arabidopsis thaliana.";
 RT Plant Mol. Biol. 30:647-653(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Columbia;
 RC MEDLINE=21016721; PubMed=11130714;
 RX Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
 RA Watanabe A., Yanai H., Ohta S., Saito S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Haberman K., Murray J., Johnson D., Rohlfing T., Nelson J.,
 RA Stoneking T., Pepin K., Splich J., Courtney L., Courtney M., Dante M.,
 RA Belter E., Cordum H., Cordes M., Muraki A., Lamat E., Latreille P.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Jarmak A., Strommalt C.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Dedila N.,
 RA Wanner-McPherson C., Wollam A., Yeakum M., Bell M., Dedila N.,
 RA Patnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kitzhoff K., Toth K., King L., Bahret A., Miller B., Maria M.,
 RA Martienssen R., McCombie M.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckert G., Wambutt R., Duesterhoeft A., Stekema W., Pohl T.,
 RA Enliar K.-D., Terry N., Hartley N., Bent E., Johnson S.,

Langham S.-A., McCullagh B., Robben J., Grymmonprez B., Zimmermann W.,
 Ramsberger U., Wedler H., Balke K., Wedler E., Peters S.,
 van Staveren M., Dirks W., Moolman P., Klein Lankhorst R.,
 RA Weitzsaecker T., Both G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gelen J., Ardiles W.,
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:823-826(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. Columbia;
 RX MEDLINE-97471969; PubMed-9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneo T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.,
 RT Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT pl clones.";
 RL DNA Res. 4:215-230(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
 CC diacylglycerol 3-phosphate.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS AND LEAVES.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAINS.
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 CC -----
 DR EMBL: D63787; BAA09856.1; -
 DR EMBL: AL133421; CAB62604.1; -
 DR EMBL: AB005249; BAB09956.1; -
 DR InterPro: IPR000756; DAGKA.
 DR InterPro: IPR001206; DAGKC.
 DR InterPro: IPR002219; DAG-PE-bind.
 DR InterPro: IPR003622; DAG_Kin_cat.
 DR Pfam: PF00609; DAGKA; 1.
 DR Pfam: PF00781; DAGKC; 1.
 DR ProDom: PD002939; DAGKA; 1.
 DR ProDom: PD005043; DAG_Kin_cat; 1.
 DR SMART: SM00109; C1; 2.
 DR SMART: SM00045; DAGKA; 1.
 DR SMART: SM00046; DAGKC; 1.
 DR PROSITE: PS00479; DAG-PE_BIND_DOM_1; FALSE_NEG.
 DR PROSITE: PS50081; DAG-PE_BIND_DOM_2; 2.
 KW Transferase; Kinase; Phorbol-ester binding; Transmembrane; Repeat.
 FT TRANSFERASE 27 48
 FT DOMAIN 95 137
 FT DOMAIN 169 212
 FT DOMAIN 359 480
 FT DOMAIN 507 664
 FT DOMAIN 509 509
 FT CONFLICT N -> T (IN REF. 1).
 SQ SEQUENCE 728 AA; 79983 MW; 9E3190721C083DE9 CR664;

Query Match 8.5%; Score 74.5; DB 1; Length 728;
 Best Local Similarity 25.7%; Pred. No. 21;
 Matches 43; Conservative 22; Mismatches 67; Indels 35; Gaps 8;

OY 8 DDGSGGSGGQGV-----SVNNEH-----NVANVDNNGGSMWAMMDYRGFAV 52
 Db 273 DGGSGGSGGQGV-----SVNNEH-----NVANVDNNGGSMWAMMDYRGFAV 52
 OY 53 TRLEFKS--CLVHKAKKA--MPSLDALDLVKEKKLOGKGGPGPPKSLRYSVPNV 108
 Db 333 TGSFOKEVYHNRSLKYLDELDP--DARPLLVTFTNKKSGAGRGDSLRLHLNLPVY 391

OY 109 DMLDKF-GKSI-----VAMCKGIPY--YMAEIOGANLIS 140
 Db 392 FELSSVGGPEVGLFLPKRVHFRVAVGSGDSTAGWIDALEKONFIS 438

RESULT 14
 MMLC-MYCTU
 ID MMLC-MYCTU STANDARD; PRT; 1146 AA.
 AC Q50585;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative membrane protein mmpL12.
 GN MMLP12 OR RV1522C OR MT1573 OR MTCY1965.06.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.D., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.,
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickley E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolova M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weisman J., Kouri H., Gill J., Mikula A.,
 RA Bishai W.,
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE MMLP FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: Z77826; CAB01394.1; -
 DR EMBL: AE007024; AAK45840.1; -
 DR TIGR: MT1573; -
 DR Tuberculist; RV1522C; -
 DR InterPro: IPR004707; ActII.
 DR InterPro: IPR000731; HMGCR/patch_57M.
 DR InterPro: IPR004869; MMLP.
 DR Pfam: PF03176; MMLP; 2.
 DR PROSITE: PS50156; SSD; 1.
 DR PROSITE: TIGR00833; actII; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSFERASE 25 45
 FT TRANSFERASE 206 226
 FT TRANSFERASE 254 274
 FT TRANSFERASE 350 350
 FT TRANSFERASE 382 402
 FT TRANSFERASE 826 846
 FT TRANSFERASE POTENTIAL.
 FT TRANSFERASE POTENTIAL.
 FT TRANSFERASE POTENTIAL.
 FT TRANSFERASE POTENTIAL.
 FT TRANSFERASE POTENTIAL.
 FT TRANSFERASE POTENTIAL.

```

Query Match Similarity 8.4%: Score 74; DB 1; Length 1146;
Best Local Similarity 20.8%: Pred. No. 40;
Matches 41: Conservative 26; Mismatches 66; Indels 64; Gaps 6

OY 9 DGNSSGSCQOQ--SVSNENHNVAVDNNGNNSMNAIWDYETGFAVRLFEKKSCTVHK 65
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 514 DQLTGGAHQADLADALAQIRREINGCAVASSSGIVNTLQAMMDLMGDKPTIRQLENAQYGR 573
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 66 MK-----KEAMPSLQAL-----DALY 81
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 574 MKAALCDNLGTVTDAEQIATWASPMVNAIENSSPVCNSDPACRTSRAQIAIYQAOQDGLL 633
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 82 KKK-----LQKGGCGCPPEKSLRYSVNENRVDNLDKFEKSIYAMCK--GIPTYMAEEL 133
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 634 RSRALAVTLQ-----QTEQVOTLARIYSTLDGQLKQVSTLKAVDGLPTKRLAQMO 684
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 134 OGANIISTSEKTSANI 150
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 685 OGANALADGSAAALAGV 701
   1 :||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 15
TP2M_DICD1
AC TP2M_DICD1 STANDARD: PRT: 1282 AA.
AC P90520:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).
GN TOB OR TOPA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=97320633; PubMed=9177484;
RA Komori K., Kuroe K., Yanagisawa K., Tanaka Y.;
RT "Cloning and characterization of the gene encoding a mitochondrially
RT localized DNA topoisomerase II in Dictyostelium discoideum. Western
RT blot analysis."
RL Biochim. Biophys. Acta 1352:63-72(1997).
CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
CC MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- DEVELOPMENTAL STAGE: PRESENT IN GROWTH PHASE AND DURING
CC DEVELOPMENT, ALTHOUGH LEVELS DECLINED AS DEVELOPMENT PROCEEDED.
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: D82024; BA011510.1; -.
DR HSSP: P06786; IBGW.
DR DictyDb: DD05117; topb.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR001241; DNA_topoisolv.
DR InterPro: IPR002205; DNA_topoisolv.

```

Query Match	8.4%	Score 74	DB 1	Length 1282
Best Local Similarity	21.7%	Pred No. 46		
Matches 31, Conservative	25	Mismatches 39	Indels 48	Gaps 6

Search completed: April 11, 2003, 16:12:02
Job time : 12.8567 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:53 ; Search time 17.7651 Seconds

(without alignments)
892.865 Million cell updates/sec

Title: US-09-821-726A-18_COPY_21_185

Perfect score: 880

Sequence: 1 DYSISVNDGSGSGGQOSV.....ISANILWILINISFCGGAEN 165

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.5	10.7	719	2 S61046	ARPI protein - yea
2	83.5	9.5	186	2 T30918	hypothetical prote
3	83	9.4	296	2 S38907	probable phosphati
4	82.5	9.4	409	2 T35118	pyruvate dehydroge
5	82.5	9.4	887	2 E81094	hypothetical prote
6	81	9.2	810	2 S69652	hypothetical prote
7	81	9.2	1338	2 T18287	protein-tyrosine k
8	80.5	9.1	263	2 T07227	NBS-LRR type resis
9	80.5	9.1	642	2 G86087	protein B0454.8 [1
10	80	9.1	568	2 JC7210	molluscan shell ma
11	79.5	9.0	227	2 T07755	disease resistance
12	78.5	8.9	887	2 E81847	pyruvate dehydroge
13	78	8.9	192	2 T02628	hypothetical prote
14	78	8.9	349	2 A85091	hypothetical prote
15	77	8.8	808	2 B97303	hypothetical prote
16	77	8.8	954	1 S20907	endo-1,4-beta-xyla
17	77	8.8	1245	2 D71613	GAF domain protein
18	76.5	8.7	764	2 H71607	hypothetical prote
19	76	8.6	1597	2 S51144	Ribi protein - yea
20	75.5	8.6	443	2 B99952	conserved hypothet
21	75	8.5	421	2 A43627	maltoase-binding pe
22	75	8.5	442	2 A54529	citramporozolite p
23	74.5	8.5	728	2 S71467	diacylglycerol kin
24	74.5	8.5	1240	2 T06404	resistance complx
25	74.5	8.5	2010	2 B71616	phosphatase (acid
26	74	8.4	244	2 A66873	transcription regu
27	74	8.4	883	2 T49781	related to mutanas
28	74	8.4	1146	2 B70723	probable mmp12 pr
29	74	8.4	1168	2 T15890	hypothetical prote

30	74	8.4	1282	2 T30577	DNA topoisomerase
31	74	8.4	2150	2 S71629	sensory transducti
32	73.5	8.4	219	2 B41886	flagellar membrane
33	73.5	8.4	1195	2 S38174	probable purine nu
34	73	8.3	414	2 S43253	alanine-glyoxylate
35	73	8.3	472	2 T24316	hypothetical prote
36	73	8.3	535	1 A44475	N-acetylglactosam
37	73	8.3	817	2 A47716	dolichyl-phosphate
38	73	8.3	1006	2 A59384	oxyluciferase/insu
39	73	8.3	1025	2 A59383	oxyluciferase/insu
40	72.5	8.2	286	2 F90006	hypothetical prote
41	72.5	8.2	375	1 G64436	N-acetyl-gamma-glu
42	72.5	8.2	476	2 B41792	homeoic protein 1
43	72.5	8.2	653	2 T02080	probable carbonate
44	72.5	8.2	753	2 D83081	probable outer mem
45	72.5	8.2	1341	2 S50366	probable membrane

ALIGNMENTS

```
RESULT 1
S61046
ARPI protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D1478; protein YDL167c
C:Species: Saccharomyces cerevisiae
C:Date: 15-Feb-1996 #sequence, revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S61046; S31139; S67719
R:Pohl, T.M.
Submitted to the EMBL Data Library, November 1995
A:Reference number: S61010
A:Accession: S61046
A:Molecule type: DNA
A:Residues: 1-719 <POH>
A:Cross-references: EMBL:267750; NID:g1061256; PIDN:CAA91570.1; PID:g1061272
R:Wehner, E.P.; Rao, E.; Brendel, M.
Mol. Gen. Genet. 237, 351-358, 1993
A:Title: Molecular structure and genetic regulation of SPA, a gene responsible for re
A:Reference number: S31138; MID:93247548; PMID:8483449
A:Accession: S31139
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492, 'N', 494-719 <WEH>
A:Cross-references: EMBL:X68020; NID:g577609; PIDN:CAA48159.1; PID:g288590
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A:Reference number: S67708
A:Accession: S67719
A:Molecule type: DNA
A:Residues: 1-719 <POH>
A:Cross-references: EMBL:274215; NID:g1431265; PIDN:CAA98741.1; PID:e253076; PID:g143
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:NRP1; ARPI
A:Cross-references: MIPS:YDL167c; SGD:S0002326
A:Map position: 4L

Query Match      10.7%; Score 94.5; DB 2; Length 719;
Best local Similarity 24.8%; Pred. No. 0.34;
Matches 39; Conservative 18; Mismatches 63; Indels 37; Gaps 5;

QY 2 YSISVNDGSGSGGQOSVSVNNEH-----VAVYDNNNGNNSWALW 44
DB 508 YNINNNINGNGNGNNGNNSNNNNHHHNGSINSNSNTNNNNNNNGNNSNCNS 567
QY 45 DYRTGFAVTRL-----FEKKSCIVHKMKKEAM-----PSLOALDLVKEKKLOGK--G 90
DB 568 NIGMGCGSNMPPRAGDMKSTCTYHFAKNVYCLRCGGKKSISGDASEFNHYIDSSTFG 627
QY 91 PGCPPEKSLRYSVNP-----RVNDLDFKGSIVAM 121
DB 628 PASRTPSNNNISVNTNGSNAGRTDGNKGRDISLM 664
```

RESULT 2

T30918

hypothetical protein D1007.14 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30918

R:Davidson, S.; Rohlfing, T.

Submitted to the EMBL Data Library, August 1999

A:Description: The sequence of *C. elegans* cosmid D1007.

A:Reference number: Z20934

A:Accession: T30918

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-186 <DAV>

A:Cross-references: EMBL:AF003151; PIDN:AB54231.1

A:Experimental source: strain Bristol N2; clone D1007

C:Genetics:

A:Map position: 1

A:Introns: 15/2; 68/2; 87/2

A:Note: D1007.14

Query Match

Best Local Similarity 39.5%; Pred. No. 0.75;

Matches 17; Conservative 8; Mismatches 15; Indels 3; Gaps 1;

QY 7 NDDGNSGGSGGQSVSVNNEHNVANVDNNNGW---NSMNLMDY 46

Db 34 NNGAGSGSGWGNANNNNNNNNGSGNNNGWGNNDWSSNYN 76

RESULT 3

S38907

probable phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - *Clostridium pasteurii*C:Species: *Clostridium pasteurianum*

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 28-Jul-2000

C:Accession: S38907

R:Meyer, J.

Submitted to the EMBL Data Library, November 1993

A:Description: Sequence of 6764 bp EcoRI-Sau3A fragment of *Clostridium pasteurianum* gene

ly M62754).

A:Reference number: S38903

A:Accession: S38907

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-296 <MEY>

A:Cross-references: EMBL:Z28353; NID:9431946; PIDN:CA82212.1; PID:9431951

C:Superfamily: *Escherichia coli* phosphatidylserine decarboxylase

C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match

Best Local Similarity 27.3%; Pred. No. 1.5;

Matches 36; Conservative 18; Mismatches 46; Indels 3; Gaps 6;

QY 20 VSVNNEHNVANVNNNGNSMNLMDYRTGFAVTRLFEEKSCIVHMKKEAMPSLQALDA 79

Db 116 IIVVNNITMNNIIOYKGT--YKLNLDLQNDISKTYEKGICIAIACPTDVRHFFLDN 173

QY 80 LVREKKLQKGPGEPPPKSLKYSNP---NRVDNL-----DKFGK---STV 119

Db 174 GICSTIKIKGN-----YYSNPDIALINKINLFCQKREMSIFNSDNFGKILYEIG 225

QY 120 AMCKG--IPTYM 129

Db 226 ATCVGSIIQTYM 237

RESULT 4

T35118

probable secreted protein - *Streptomyces coelicolor*C:Species: *Streptomyces coelicolor*

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 08-Sep-2000

C:Accession: T35118

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, March 1998

A:Reference number: Z21568

A:Accession: T35118

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-409 <SEE>

A:Cross-references: EMBL:AL022268; PIDN:CA18335.1; GSPD:GN00070; SCOEDB:SC4H2.19C

A:Experimental source: strain A3(2)

C:Genetics:

A:Superfamily: *Streptomyces coelicolor* probable secreted protein SC4H2.19C

Query Match

Best Local Similarity 21.1%; Pred. No. 2.6;

Matches 39; Conservative 21; Mismatches 74; Indels 51; Gaps 7;

QY 3 SISVNDGNSGGGQSVSVNNEHNVANVDN--NNGNSMN-----AL 43

Db 54 SASAADGNGGIRIPDDIKOKLKEHGIDVDDMKNGAMKMKDDWLREADQFVNPIEGL 113

QY 44 WDYRTGFAVTRLFEEKSCIVHMKKEAMPSLQALDALYKCKLQK-KPGGPPPKSLKYS 102

Db 114 WD-----PDRMRDAEPPDOEVDENDISGQGVTPDEPAPEAE 151

QY 103 VNPBRV-DNLDPFGKSIYAMCKGIPTVAAEEIQQ-----ANLISYKCKISANIL--WI 153

Db 152 AVPAKYHDNMAATAGKLLFPSPKSGMWCATYVVKDPAHFGKSNMVTAGCHVAGSGGTY 211

QY 154 LNISF 158

Db 212 RNIAF 216

RESULT 5

E81094

pyruvate dehydrogenase, E1 component NMB1341 [imported] - *Neisseria meningitidis* (strC:Species: *Neisseria meningitidis*

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: E81094

R:Teitelin, H.; Saunders, N.J.; Haidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maslignani, V.; Pizze, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A:Reference number: AB1000; MUID:20175753; PMID:10710307

A:Accession: E81094

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-887 <TEF>

A:Cross-references: GB:AE002482; GB:AE002098; NID:97226577; PIDN:AAE41716.1; PID:97222

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1341

C:Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding doma

Query Match

Best Local Similarity 24.1%; Pred. No. 7.2;

Matches 41; Conservative 24; Mismatches 60; Indels 45; Gaps 9;

QY 9 DGNSGGSGGQSVSVNNEHNVANVDNNNGN---SMNLMDYRTGFAVTRLFEPK-KSCIV 63

Db 264 DGPYRGNGK--IIQELGKNFGA---GMNVYKVIWGRWD-----RLAKKRDGIL 309

QY 64 HKMKKEAM-----PSLQALDALYKCKLQKGGGPPPKSLRY 101

Db 310 RQRMEECLDGDGYQYKSKDAVYREHFENPELAKALVADMDQELMALNRGSHDPQKY-Y 368

QY 102 SVNPNRVNDLPFGKSIYAMCKGIPTV-MAEIIQGANLISSEKISANI 150

Db 369 NAYDRANHAD--GKPTVIAKTIKGYGMGASGCONVAAHQAQKWKDASL 416


```

0Y 49 GFAATRLFEK--KSCIVHKMKKEAMPs-----LQALDALVKEKKLQGGCGGPPPSLR 100
Dd 379 GLRIEALKIKLVKAVPIDSLALDPPRLVNGDTASINAVIK-----PDNATNGLT 430
0Y 101 YSVNPNRYNDLNRKGSIVAMCKGIPYMAEEIOGA-----NLISYSEKCI 146
Dd 431 WTSSDNKKIISVNSGK-ITGINKIGIATITTAASNDGSKKASCCTITVNDPNNNIYTFKDSNL 489
0Y 147 SANILMIIN 155
Dd 490 EAEVRKCIIN 498

```

QY 9 DCGSGGSCGOOSV-----SYNNEHNVAANDNNNGNSW----NALWDYRT 48
|| : : : | : : || : :
Db 324 DGEAGTGGKGLRYEAIIRIKLVMPGYSEIYSHVQN---GMGNWVSDDGEAGTGGR- 378

Mon Apr 14 14:02:08 2003

us-09-821-726a-18_copy_21_185.rapb

GenCore version 5.1.4_p5.4578
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OW protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 16.4192 seconds
(without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726a-18_COPY_21_185
Perfect score: 880
Sequence: 1 DYSISVNDGNSGSGQOSV.....ISANIIWILNISFGGIAEN 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEM_PUB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCIT_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NPM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US07_NPM_PUB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCITUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US09_NEM_PUB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US10_NEM_PUB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	687	78.1	185	US-09-992-598-211	Sequence 211, App
2	687	78.1	185	US-09-989-293A-211	Sequence 211, App
3	687	78.1	185	US-09-990-444-211	Sequence 211, App
4	687	78.1	185	US-10-001-054-14	Sequence 211, App
5	687	78.1	185	US-09-989-730-211	Sequence 211, App
6	687	78.1	185	US-09-990-436-211	Sequence 211, App
7	687	78.1	185	US-09-991-181-211	Sequence 211, App
8	687	78.1	185	US-09-993-687-211	Sequence 211, App
9	687	78.1	185	US-09-989-734-211	Sequence 211, App
10	687	78.1	185	US-09-997-653-211	Sequence 211, App
11	687	78.1	185	US-09-993-438-211	Sequence 211, App
12	687	78.1	185	US-09-990-438-211	Sequence 211, App
13	687	78.1	185	US-09-990-562-211	Sequence 211, App
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ALIGNMENTS

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Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PJC20
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PRIOR FILING DATE: 1998-07-09

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RESULT 2
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Sequence 211, Application US/09989293A
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC66
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;
Best Local Similarity 73.3%; Pred. No. 3.6e-65;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

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Db 21 NVNIVNDNNDNAGSGGQSVSYVNEHNVANVDNNGMNSNALMDYRTGFAVTRLEPKKT 80
QY 61 CIVHMKKEAMPSLQALDALVKEKLGKPGGPPKSLRYSVNPKNVDLDEFGKSIVA 120
Db 81 CIVHMKKEAMPSLQALDALVKEKLGKPGGPPKSLRYSVNPKNVDLDEFGKSIVA 140
QY 121 MCKGPTMAEITOGANLISYSEKCSANILMTLNTSFCGGIEN 165
Db 141 MCKGPTMAEITOGANLISYSEKCSANILMTLNTSFCGGIEN 185

RESULT 4
US-09-990-444-211
Sequence 211, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-16
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5 Prior Filing Date: 1998-07-01
6 Prior Application Number: 60/091519
7 Prior Filing Date: 1998-07-02
8 Prior Application Number: 60/091626
9 Prior Filing Date: 1998-07-02
10 Prior Application Number: 60/091633
11 Prior Filing Date: 1998-07-02
12 Prior Application Number: 60/091978
13 Prior Filing Date: 1998-07-07
14 Prior Application Number: 60/091982
15 Prior Filing Date: 1998-07-07
16 Prior Application Number: 60/092182
17 Prior Filing Date: 1998-07-09
18
19 Query Match 78.1%; Score 687; DB 9; Length 185;
20 Best Local Similarity 73.3%; Pred. No. 3,6e-65;
21 Matches 121; Conservative % 22; Mismatches 22; Indels 0; Gaps
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23 Oy 1 DYSTSYNDGSGSGSGGOSVSNNEHNVANVNDNNNGNSMALMDYRFGAVTLRFKKS 60
24 Db 21 NNTNVNDNNNAGSGGOSVSNNEHNVANVNDNNNGMDSNMSINDYGNFATYLPFKKT 80
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26 Oy 61 CIVHMKREAPSLQALDALVKKERKLGKGGPPKSLRYSVNPBNVDLIDKFGKIVA 120
27 Db 81 CIVHMKNEVWPSIQSLDALVKKERKLGKGGPPKGLMYSVNPKNVYDLISKFGKNIAN 140
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29 Oy 121 MCKGIPTYMAEBIGCANLISSEKCIANSNIIILINISFGGIAEN 165
30 Db 141 MCKGIPTYMAEBMGEASLFEYSGCTYTSVLMIWDISFGGTVEN 185
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32 RESULT 5
33 US-10-001-054-14
34 Sequence 14, Application US/10001054
35 Publication No. US20020192209A1
36 GENERAL INFORMATION:
37 APPLICANT: Genentech, Inc.
38 APPLICANT: Baker, Kevin
39 APPLICANT: Goddard, Audrey
40 APPLICANT: Gurney, Austin
41 APPLICANT: Hebert, Carolyn
42 APPLICANT: Henzel, William
43 APPLICANT: Kabakoff, Rhona
44 APPLICANT: Shelton, David
45 APPLICANT: Smith, Victoria
46 APPLICANT: Watanabe, Colin
47 APPLICANT: Wood, William
48 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
49 FILE REFERENCE: P3034R1PCT
50 CURRENT APPLICATION NUMBER: US/10/001,054
51 CURRENT FILING DATE: 2001-11-30
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53 Prior Filing Date: 1997-09-17
54 Prior Application Number: 60/079689
55 Prior Filing Date: 1998-03-27
56 Prior Application Number: 60/079920
57 Prior Filing Date: 1998-03-30
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59 Prior Filing Date: 1998-04-24
60 Prior Application Number: 60/083545
61 Prior Filing Date: 1998-04-29
62 Prior Application Number: 60/085145
63 Prior Filing Date: 1998-05-12
64 Prior Application Number: 60/087607
65 Prior Filing Date: 1998-06-02
66 Prior Application Number: 60/088858
67 Prior Filing Date: 1998-06-11
68 Prior Application Number: 60/090691
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match
Best Local Similarity 78.1%; Score 687; DB 9; Length 185;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

Qy 1 DYSISVNDGNSGSGQSVSYNNEHNVANYDNNNGHNSMALWDYRTGFAVTRLEERKS 60
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Db 141 MCKGIPTYMAEIEIOGANLISSEKCSANILITILITISFCGIAEN 185

RESULT 7
US-09-990-436-211

Sequence 211, Application US/09990436
Publication No. US20020198148A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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72	PRIOR FILING DATE: 1998-06-26
73	PRIOR APPLICATION NUMBER: 60/091360

QY 1 DYSIVNDNGSGGGGQGVSYVNEHNVAVDNNGNGSMNALMDYRTGEAYTRLEPKS 60
Db 21 NININAVDNDNNAGGGQGVSYVNEHNVAVDNNGNGSMNALMDYRTGEAYTRLEPKS 80
QY 61 CIVHKMKREAMPDIALALVYERKKLQCGPGPPPKSLRYSVNPNRVNDINDKFEKSIYA 120
Db 81 CIVHKMKNEVAPSDLSLALYERKKLQCGPGPPPKSLRYSVNPNRKVDLDSFGKNIAN 140
QY 121 MCKGIPYMAEIOGANTISYSEKISIANIILILNISFCGJIAEN 165
Db 141 MCKGIPYMAEIOGANTISYSEKISIANIILNISFCGJIAEN 185

Sequence 211, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashland Inc.

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Collin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C53
 CURRENT APPLICATION NUMBER: US/09/991,181
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17

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7 PRIOR APPLICATION NUMBER: 60/075945
8 PRIOR FILING DATE: 1998-02-25
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10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/083332
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68 PRIOR FILING DATE: 1998-06-11
69 PRIOR APPLICATION NUMBER: 60/0889105
70 PRIOR FILING DATE: 1998-06-12
71 PRIOR APPLICATION NUMBER: 60/089440
72 PRIOR FILING DATE: 1998-06-16
73 PRIOR APPLICATION NUMBER: 60/089512

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PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09

Query Match      78.1%;      Score 687;      DB 9;      Length 185;
Best Local Similarity 73.3%;      Pred. No. 3,6e-65;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0

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1 RESULT 9
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4 ; Sequence 211, Application US/09993687
5 ; Publication No. US20020198149A1
6
7 GENERAL INFORMATION:
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9 APPLICANT: Ashkenazi, Avi J.
10
11 APPLICANT: Baker, Kevin P.
12
13 APPLICANT: Bolstein, David
14
15 APPLICANT: Desnoyers, Luc
16
17 APPLICANT: Eaton, Dan L.
18
19 APPLICANT: Ferrara, Napoleone
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21 APPLICANT: Fong, Sherman
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23 APPLICANT: Gerber, Hanspeter
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25 APPLICANT: Gerlitsen, Mary E.
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27 APPLICANT: Goddard, Audrey
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29 APPLICANT: Godowski, Paul J.
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31 APPLICANT: Grimaldi, J. Christopher
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33 APPLICANT: Gurney, Austin L.
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35 APPLICANT: Kljavin, Ivar J.
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37 APPLICANT: Napier, Mary A.
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39 APPLICANT: Pan, James
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41 APPLICANT: Paoni, Nicholas F.
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43 APPLICANT: Roy, Margaret Ann
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45 APPLICANT: Stewart, Timothy A.
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47 APPLICANT: Tumas, Daniel
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49 APPLICANT: Watanabe, Colin K.
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51 APPLICANT: Williams, P. Mickey
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53 APPLICANT: Wood, William I.
54
55 APPLICANT: Zhang, Zemin
56
57 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
58
59 FILE REFERENCE: P2730PIC11
60
61 CURRENT APPLICATION NUMBER: US/09/993,687
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63 CURRENT FILING DATE: 2002-11-14
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67 PRIOR FILING DATE: 1997-06-16
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69 PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-06-16

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72	PRIOR FILING DATE: 1998-06-12
73	PRIOR APPLICATION NUMBER: 60/089440

Query Match	78.1%;	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%;	Pred. No. 3.6e-65;		
Matches 121;	Conservative 22;	Mismatches 22;	Indels 0;	Gaps 0

RESULT 11
US-09-997-653-211

PRIOR APPLICATION NUMBER: 60/090431	Sequence 211, Application US/09997653
PRIOR FILING DATE: 1998-06-24	Publication No. US20030008297A1
PRIOR APPLICATION NUMBER: 60/090435	GENERAL INFORMATION:
PRIOR FILING DATE: 1998-06-24	APPLICANT: Ashkenazi, Avi J.
PRIOR APPLICATION NUMBER: 60/090444	APPLICANT: Baker, Kevin P.
PRIOR FILING DATE: 1998-06-24	APPLICANT: Botstein, David
PRIOR APPLICATION NUMBER: 60/090445	APPLICANT: Desnoyers, Luc
PRIOR FILING DATE: 1998-06-24	APPLICANT: Eaton, Dan L.
PRIOR APPLICATION NUMBER: 60/090472	APPLICANT: Ferrara, Napoleone
PRIOR FILING DATE: 1998-06-24	APPLICANT: Fong, Sherman
PRIOR APPLICATION NUMBER: 60/090535	APPLICANT: Gerber, Hanspeter
PRIOR FILING DATE: 1998-06-24	APPLICANT: Gerlitsen, Mary E.
PRIOR APPLICATION NUMBER: 60/090540	APPLICANT: Goddard, Audrey
PRIOR FILING DATE: 1998-06-24	APPLICANT: Godowski, Paul J.
PRIOR APPLICATION NUMBER: 60/090542	APPLICANT: Grimaldi, J. Christopher
PRIOR FILING DATE: 1998-06-24	APPLICANT: Gurney, Austin L.
PRIOR APPLICATION NUMBER: 60/090557	APPLICANT: Kijaviri, Ivar J.
PRIOR FILING DATE: 1998-06-24	APPLICANT: Napier, Mary A.
PRIOR APPLICATION NUMBER: 60/090676	APPLICANT: Pan, James
PRIOR FILING DATE: 1998-06-25	APPLICANT: Paoni, Nicholas F.
PRIOR APPLICATION NUMBER: 60/090678	APPLICANT: Roy, Margaret Ann
PRIOR FILING DATE: 1998-06-25	APPLICANT: Stewart, Timothy A.
PRIOR APPLICATION NUMBER: 60/090690	APPLICANT: Tumas, Daniel
PRIOR FILING DATE: 1998-06-25	APPLICANT: Watanabe, Colin K.
PRIOR APPLICATION NUMBER: 60/090694	APPLICANT: Williams, P. Mickey
PRIOR FILING DATE: 1998-06-25	APPLICANT: Wood, William I.
PRIOR APPLICATION NUMBER: 60/090695	APPLICANT: Zhang, Zemin
PRIOR FILING DATE: 1998-06-25	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
PRIOR APPLICATION NUMBER: 60/090696	TITLE OF INVENTION: Acids Encoding the Same
PRIOR FILING DATE: 1998-06-25	FILE REFERENCE: P2730P1C38
PRIOR APPLICATION NUMBER: 60/090862	CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR FILING DATE: 1998-06-26	CURRENT FILING DATE: 2001-11-15
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73	PRIOR FILING DATE: 1998-06-12

1	PRIOR APPLICATION NUMBER: 60/089440
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30	PRIOR FILING DATE: 1998-06-19
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32	PRIOR FILING DATE: 1998-06-22
33	PRIOR APPLICATION NUMBER: 60/090252
34	PRIOR FILING DATE: 1998-06-22
35	PRIOR APPLICATION NUMBER: 60/090254
36	PRIOR FILING DATE: 1998-06-22
37	PRIOR APPLICATION NUMBER: 60/090349
38	PRIOR FILING DATE: 1998-06-23
39	PRIOR APPLICATION NUMBER: 60/090355
40	PRIOR FILING DATE: 1998-06-23
41	PRIOR APPLICATION NUMBER: 60/090429
42	PRIOR FILING DATE: 1998-06-24
43	PRIOR APPLICATION NUMBER: 60/090431
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/090435
46	PRIOR FILING DATE: 1998-06-24
47	PRIOR APPLICATION NUMBER: 60/090444
48	PRIOR FILING DATE: 1998-06-24
49	PRIOR APPLICATION NUMBER: 60/090445
50	PRIOR FILING DATE: 1998-06-24
51	PRIOR APPLICATION NUMBER: 60/090472
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/090535
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/090540
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/090542
58	PRIOR FILING DATE: 1998-06-24
59	PRIOR APPLICATION NUMBER: 60/090557
60	PRIOR FILING DATE: 1998-06-24
61	PRIOR APPLICATION NUMBER: 60/090675
62	PRIOR FILING DATE: 1998-06-25
63	PRIOR APPLICATION NUMBER: 60/090673
64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090690
66	PRIOR FILING DATE: 1998-06-25
67	PRIOR APPLICATION NUMBER: 60/090695
68	PRIOR FILING DATE: 1998-06-25
69	PRIOR APPLICATION NUMBER: 60/090696
70	PRIOR FILING DATE: 1998-06-25
71	PRIOR APPLICATION NUMBER: 60/090862
72	PRIOR FILING DATE: 1998-06-25

Query Match	78.1%;	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%;	Pred. No. 3.6e-65;		
Matches 121;	Conservative 22;	Mismatches 0;	Gaps 0;	

RESULT 12
US-09-993-667-21:

```

; Sequence 211, Application US/099993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:

```

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C4
 CURRENT APPLICATION NUMBER: US/09/993,667
 CURRENT FILING DATE: 2001-11-14

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PRIORITY APPLICATION NUMBER: 60/09863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match Best Local Similarity 78.1%; Score 687; DB 9; Length 185;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSTSVNDGSGGGGOSVSYNNEHNAVNNNGNWNLMNYRTGFATRLFEKS 60
DB 21 NYNINVNDNNAGSGOQSVSNNHHNVNNGWDSNSIMWDGNFATRLFOKKT 80
QY 61 CIVHKMKAMPISLDALVEKKLKGPGPKPSLRYSVPNRVNLDKFGSKIVA 120
DB 81 CIVHKMKEVMPISDLSDALVEKKLKGGPGPPKGLMSVNPKNKVDLKFEGNIAN 140
QY 121 MCKGIPTMAEIGCANISYESEKANSIIMIILNISFCGJAEN 165
DB 141 MCGRIPITMAEEMBASLFYSGTCYTTSVLMTIVDISFCGDIVEN 185

RESULT 12 US-09-993-667-211
Sequence 211, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC4
CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14

```


Query Match	78.1%	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%	Pred. No. 3, 6e-65;		
Matches 12;	Conservative 22;	Mismatches 22;	Indels 0;	Gaps 0

RESULT 13
US-09-990-438-211

US 09990438
; Sequence 211, Application US/09990438
; Publication No. US20030027754A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: EALCOH, Dan E.
ADDRESSEE: Barbara Napole

APPLICANT: FELDA, Napos
ADDICANT: Food Sherman

APPLICANT: Gerber, Hanspet

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, J. Chr

APPLICANT: Gurney, Austin

APPLICANT: Kljavin, Ivar J

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas

APPLICANT: ROY, MARGARET

APPLICANT: Thomas Steward, Jr.

APPLICANT: Watanabe, Col

APPLICANT: Williams, P. M.

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secret

TITLE OF INVENTION: Acid:

FILE REFERENCE: P2730P1C3

CURRENT APPLICATION NUMBER

1	PRIOR APPLICATION NUMBER: 60/0891105
2	PRIOR FILING DATE: 1998-06-12
3	PRIOR APPLICATION NUMBER: 60/0894400
4	PRIOR FILING DATE: 1998-06-16
5	PRIOR APPLICATION NUMBER: 60/0895121
6	PRIOR FILING DATE: 1998-06-16
7	PRIOR APPLICATION NUMBER: 60/0895141
8	PRIOR FILING DATE: 1998-06-16
9	PRIOR APPLICATION NUMBER: 60/0895522
10	PRIOR FILING DATE: 1998-06-17
11	PRIOR APPLICATION NUMBER: 60/0895358
12	PRIOR FILING DATE: 1998-06-17
13	PRIOR APPLICATION NUMBER: 60/0895958
14	PRIOR FILING DATE: 1998-06-17
15	PRIOR APPLICATION NUMBER: 60/0895959
16	PRIOR FILING DATE: 1998-06-17
17	PRIOR APPLICATION NUMBER: 60/0896000
18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/0896533
20	PRIOR FILING DATE: 1998-06-17
21	PRIOR APPLICATION NUMBER: 60/0898001
22	PRIOR FILING DATE: 1998-06-18
23	PRIOR APPLICATION NUMBER: 60/0899007
24	PRIOR FILING DATE: 1998-06-18
25	PRIOR APPLICATION NUMBER: 60/0899008
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31	PRIOR APPLICATION NUMBER: 60/0899552
32	PRIOR FILING DATE: 1998-06-19
33	PRIOR APPLICATION NUMBER: 60/0902466
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35	PRIOR APPLICATION NUMBER: 60/0902552
36	PRIOR FILING DATE: 1998-06-22
37	PRIOR APPLICATION NUMBER: 60/0902554
38	PRIOR FILING DATE: 1998-06-22
39	PRIOR APPLICATION NUMBER: 60/0903039
40	PRIOR FILING DATE: 1998-06-23
41	PRIOR APPLICATION NUMBER: 60/0903555
42	PRIOR FILING DATE: 1998-06-23
43	PRIOR APPLICATION NUMBER: 60/0904299
44	PRIOR FILING DATE: 1998-06-24
45	PRIOR APPLICATION NUMBER: 60/0904331
46	PRIOR FILING DATE: 1998-06-24
47	PRIOR APPLICATION NUMBER: 60/0904335
48	PRIOR FILING DATE: 1998-06-24
49	PRIOR APPLICATION NUMBER: 60/0904444
50	PRIOR FILING DATE: 1998-06-24
51	PRIOR APPLICATION NUMBER: 60/0904445
52	PRIOR FILING DATE: 1998-06-24
53	PRIOR APPLICATION NUMBER: 60/0904712
54	PRIOR FILING DATE: 1998-06-24
55	PRIOR APPLICATION NUMBER: 60/0905355
56	PRIOR FILING DATE: 1998-06-24
57	PRIOR APPLICATION NUMBER: 60/0905400
58	PRIOR FILING DATE: 1998-06-24
59	PRIOR APPLICATION NUMBER: 60/0905442
60	PRIOR FILING DATE: 1998-06-24
61	PRIOR APPLICATION NUMBER: 60/0905557
62	PRIOR FILING DATE: 1998-06-24
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65	PRIOR APPLICATION NUMBER: 60/0906768
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67	PRIOR APPLICATION NUMBER: 60/0906950
68	PRIOR FILING DATE: 1998-06-25
69	PRIOR APPLICATION NUMBER: 60/0906954
70	PRIOR FILING DATE: 1998-06-25
71	PRIOR APPLICATION NUMBER: 60/0906955
72	PRIOR FILING DATE: 1998-06-25
73	PRIOR APPLICATION NUMBER: 60/0906966
74	PRIOR FILING DATE: 1998-06-25
75	PRIOR APPLICATION NUMBER: 60/0906966

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;
Best Local Similarity 73.3%; Pred. No. 3,6e-65;
Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

QY 1 DYSTVNDGSGGSGGGSVNNHNVANNVNNNGMSMNLMDYRIGFAVTRLEPKS 60
DB 21 NYNINVDNNDNAGSGGGSVNNHNVANNVNNNGMSMNLMDYRIGFAVTRLEPKS 80
QY 61 CIVHMKKEAMPSTLADALVYKCKLGGKPGPPKSLRYSVNPNDVNDLKEFGKSIVA 120
DB 81 CIVHMKKEAMPSTLADALVYKCKLGGKPGPPKSLRYSVNPNDVNDLKEFGKSIVA 140
QY 121 MCKGPTTMAEPIQGANLISYSEKISNIIILNISCQGAEN 165
DB 141 MCKGPTTMAEPIQGANLISYSEKISNIIILNISCQGAEN 185

RESULT 14
US-09-990-562-211
Sequence 211, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, U. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC18

CURRENT APPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088555
PRIOR FILING DATE: 1998-06-09
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PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876

Query Match	78.1%;	Score 687;	DB 9;	Length 185;
Best Local Similarity	73.3%;	Pred. No. 3.6e-65;		
Matches 121; Conservative	22;	Mismatches 22;	Indels 0;	Gaps 0;

RESULT 15
US-09-997-428-211

Sequence 211, Application us/09997428
Publication No. US20030027162A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2730P1C44
 CURRENT APPLICATION NUMBER: US/09/997,428
 CURRENT FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
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 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
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 PRIOR FILING DATE: 1998-06-04
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 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
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 PRIOR APPLICATION NUMBER: 60/088202
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 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
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; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090696
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
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 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 78.1%; Score 687; DB 9; Length 185;
 Best Local Similarity 73.3%; Pred. No. 3.6e-65;
 Matches 121; Conservative 22; Mismatches 22; Indels 0; Gaps 0;

OY 1 DYSISVNDGSGGSGQSVSVNHNANVNDNNNGWSMNLMDYRTGFAVTRLEPKS 60
 Db 21 NNNINVDNDNNAGSGQSVSVNHNANVNDNNNGWSMNLMDYRTGFAVTRLEPKS 80
 OY 61 CIVHKMKKEAMPISQALDALVKEKKLOGKPGPPKSLRYSVNPBNVDNLDPKFSIYA 120
 Db 81 CIVHKMKKEVVPISQSLDALVKEKKLOGKPGPPKGLMYSVNPNKYDDLKSGKNTAN 140
 OY 121 MCKGIPITYMAEIOGANLISYSEKICISANIITLILNISFCGGIAEN 165
 Db 141 MCRGIPITYMAEIOGANLISYSEKICISANIITLILNISFCGGIAEN 185

Search completed: April 11, 2003, 16:17:46
 Job time : 17.4192 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 ; Search time 11.7847 Seconds

(without alignments)
474.899 Million cell updates/sec

Title: US-09-821-726A-13_COPY_78_119

Perfect score: 221

Sequence: 1 KKTCTVHKMKKEVMPISQSL.....LVKEKKLQKGGPGPPPKGL 42

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	216	97.7	185	20	AAW99667
2	216	97.7	185	21	AAW99667
3	216	97.7	185	21	AAW99667
4	216	97.7	185	21	AAW99667
5	216	97.7	185	22	AAW99667
6	216	97.7	185	22	AAW99667
7	216	97.7	185	23	AAW99667
8	216	97.7	185	23	AAW99667
9	216	97.7	185	23	AAW99667
10	216	97.7	185	23	AAW99667

11	216	97.7	194	19	AAW69974	Cancer associated
12	216	97.7 <td>194 <td>20 <td>AAW76591</td> <td>Human ovarian tumor</td> </td></td>	194 <td>20 <td>AAW76591</td> <td>Human ovarian tumor</td> </td>	20 <td>AAW76591</td> <td>Human ovarian tumor</td>	AAW76591	Human ovarian tumor
13	137	62.0	184	23	ABP09922	Human ORFX protein
14	62.5	28.3	103	21	AAW41048	Human ORFX ORF812
15	62.5	28.3	103	21	ABP35077	Human ORF4050 prot
16	62.5	28.3	103	22	AAW03592	Human DNA modifica
17	62.5	28.3	103	22	AAW94309	Human protein sequ
18	59.5	26.9	269	20	AAW43915	Human protein kina
19	59.5	26.9	269	20	AAW43917	Human protein kina
20	59.5	26.9	321	22	AAW99842	Novel human kinase
21	59.5	26.9	540	22	ABG22922	Novel human kinase
22	59.5	26.9	696	21	AAW19564	Rat protein kinase
23	59.5	26.9	697	9	AAW82018	Protein kinase C-I
24	59.5	26.9	697	22	AAW79730	Human protein SEQ
25	59.5	26.9	730	22	AAW79730	Human protein SEQ
26	58	26.2	555	22	AAW16208	Human novel secret
27	58	26.2	555	22	AAW16621	Human novel secret
28	58	26.2	707	23	AAW93371	Human bromodomain-
29	58	26.2	862	23	AAW73380	Human pleckstrin h
30	58	26.2	898	23	AAW73379	Human pleckstrin h
31	58	26.2	898	23	AAW73396	Human pleckstrin h
32	58	26.2	1039	23	AAW73398	Human pleckstrin h
33	58	26.2	1041	23	AAW73383	Human pleckstrin h
34	58	26.2	1416	22	ABW50153	Human transcriptio
35	58	26.2	306	22	AAW93026	Human protein sequ
36	57.5	26.0	1633	23	AAW78407	Amino acid sequenc
37	57.5	26.0	108	22	AAW08592	Human polypeptide
38	57	25.8	467	20	AAW81634	GABA-gated chlorid
39	57	25.8	496	20	AAW81633	Human polypeptide
40	56.5	25.6	127	22	AAW07630	Human polypeptide
41	56.5	25.6	464	22	ABW61748	Drosophila melanog
42	56.5	25.6	222	22	ABW70836	Human polypeptide
43	56	25.3	128	22	AAW03204	Human polypeptide
44	55.5	25.1	147	22	AAW06887	Human polypeptide
45	55.5	25.1	147	22	AAW06887	Human polypeptide

ALIGNMENTS

RESULT 1
AAW99667
ID AAW99667 standard; Protein: 185 AA.
XX
AC AAW99667;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human secreted protein clone eJ90_5 protein.
XX
KW Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokine; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.
XX
OS Homo sapiens.
XX
PN W09907840-A1.
XX
PD 18-FEB-1999.
XX
PE 06-AUG-1998; 98W0-US16318.
XX
PR 04-AUG-1998; 98US-0130189.
XX
PA 06-AUG-1997; 97US-0906708.
XX
PM (GENY) GENETICS INST INC.
XX
PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI Merberg D, Racle LA, Steininger RJ, Treacy M;
XX
DR WPI: 1999-167419/14.

DR N-PSDB: AAX19493.
XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
XX Claim 34; Page 98-99; 107pp; English.
XX
CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activating/inhibiting activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
SQ Sequence 185 AA:
XX
Query Match 97.7%; Score 216; DB 20; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 42
Db 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 119
XX
RESULT 2
AAB24067
ID AAB24067 standard; protein; 185 AA.
XX
AC AAB24067;
XX
DT 29-JAN-2001 (first entry)
DE Human PRO1005 protein sequence SEQ ID NO:34.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypohalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocellic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US00376.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX

DR WPI: 2000-572270/53.
DR N-PSDB: AAC58377.
XX
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
XX Claim 61; Fig 22; 286pp; English.
XX
XX The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1135, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds maybe used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glial, astrocytal, hypohalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocellic disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 185 AA:
XX
Query Match 97.7%; Score 216; DB 21; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 42
Db 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPKGL 119
XX
RESULT 3
AAY87272
ID AAY87272 standard; protein; 185 AA.
XX
AC AAY87272;
XX
DT 11-MAY-2000 (first entry)
DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.
XX
XX Human signal peptide containing protein: HSP; diagnosis: cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
KW antiastrumatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
PN WO200000610-A2.
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PI 26-JUN-1998; 98US-0090762.
PI 31-JUL-1998; 98US-0094983.
XX

PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
PI Lal P, Tang YT, Gorjone GA, Corley NC, Guegler KJ, Baughn MR;
PI Axelblom IE, Au-Young J, Yae H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR N-PSDB; AA298157.
PT
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
XX
XX Claim 1; Page 193-194; 327pp; English.
XX
XX AA298109 to AA298242 encode AAY67224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
XX neuroprotective, cardiovascular and antiasthmatic activities, and can
XX be used in gene therapy. HSPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense,
XX triplex-forming or ribozyme therapeutics, for detecting related sequences
XX or genetic variations, and for chromosomal mapping. HSP are also used to
XX raise specific antibodies (Ab) and to screen for agonists and
XX antagonists (potential therapeutic agents). Ab are used to diagnose, or
XX monitor, HSP-related diseases (in usual immunoassays), as therapeutic
XX antagonists, in competitive drug screens, and for purification of HSP
XX from natural sources.
XX
XX Sequence 185 AA:
SO
Query Match 97.7%, Score 216, DB 21; Length 185;
Best local similarity 97.6%; Pred. No. 2,4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KKTCTVHKMKKEMPSIOSIALVKEKKLOGKPGGPPPKGL 42
DB 78 KKTCTVHKMKKEMPSIOSIALVKEKKLOGKPGGPPPKGL 119
RESULT 4
AAY66686
ID AAY66686 standard: protein: 185 AA.
XX
XX AAY66686;
AC
XX
XX 05-APR-2000 (first entry)
DT
XX
XX Membrane-bound protein PRO1005.
DE
XX
XX Membrane-bound polypeptide: PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
OS
XX Homo sapiens.
XX
XX WO963088-A2.
PN
XX
XX 09-DEC-1999.
PD
XX

PE 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
XX 02-JUN-1998; 98US-0087609.
XX 02-JUN-1998; 98US-0087759.
XX 03-JUN-1998; 98US-0087827.
XX 04-JUN-1998; 98US-0088021.
XX 04-JUN-1998; 98US-0088025.
XX 04-JUN-1998; 98US-0088028.
XX 04-JUN-1998; 98US-0088029.
XX 04-JUN-1998; 98US-0088030.
XX 04-JUN-1998; 98US-0088033.
XX 04-JUN-1998; 98US-0088326.
XX 05-JUN-1998; 98US-0088167.
XX 05-JUN-1998; 98US-0088207.
XX 05-JUN-1998; 98US-0088212.
XX 05-JUN-1998; 98US-0088217.
XX 09-JUN-1998; 98US-0088655.
XX 10-JUN-1998; 98US-0088722.
XX 10-JUN-1998; 98US-0088730.
XX 10-JUN-1998; 98US-0088734.
XX 10-JUN-1998; 98US-0088738.
XX 10-JUN-1998; 98US-0088740.
XX 10-JUN-1998; 98US-0088741.
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XX 10-JUN-1998; 98US-0088824.
XX 10-JUN-1998; 98US-0088825.
XX 10-JUN-1998; 98US-0088826.
XX 11-JUN-1998; 98US-0088858.
XX 11-JUN-1998; 98US-0088861.
XX 11-JUN-1998; 98US-0088863.
XX 11-JUN-1998; 98US-0088876.
XX 12-JUN-1998; 98US-0089090.
XX 12-JUN-1998; 98US-0089105.
XX 16-JUN-1998; 98US-0089440.
XX 16-JUN-1998; 98US-0089512.
XX 16-JUN-1998; 98US-0089514.
XX 17-JUN-1998; 98US-0089532.
XX 17-JUN-1998; 98US-0089538.
XX 17-JUN-1998; 98US-0089598.
XX 17-JUN-1998; 98US-0089599.
XX 17-JUN-1998; 98US-0089600.
XX 17-JUN-1998; 98US-0089653.
XX 18-JUN-1998; 98US-0089801.
XX 18-JUN-1998; 98US-0089907.
XX 18-JUN-1998; 98US-0089908.
XX 19-JUN-1998; 98US-0089947.
XX 19-JUN-1998; 98US-0089948.
XX 19-JUN-1998; 98US-0089952.
XX 22-JUN-1998; 98US-0090246.
XX 22-JUN-1998; 98US-0090252.
XX 22-JUN-1998; 98US-0090254.
XX 23-JUN-1998; 98US-0090349.
XX 23-JUN-1998; 98US-0090355.
XX 24-JUN-1998; 98US-0090429.
XX 24-JUN-1998; 98US-0090431.
XX 24-JUN-1998; 98US-0090435.
XX 24-JUN-1998; 98US-0090444.
XX 24-JUN-1998; 98US-0090445.
XX 24-JUN-1998; 98US-0090461.
XX 24-JUN-1998; 98US-0090472.
XX 24-JUN-1998; 98US-0090535.
XX 24-JUN-1998; 98US-0090538.
XX 24-JUN-1998; 98US-0090540.
XX 24-JUN-1998; 98US-0090557.
XX 25-JUN-1998; 98US-0090676.
XX 25-JUN-1998; 98US-0090678.
XX 25-JUN-1998; 98US-0090688.
XX 25-JUN-1998; 98US-0090690.
XX 25-JUN-1998; 98US-0090691.
XX 25-JUN-1998; 98US-0090694.

PR 25-JUN-1998; 98US-0090695.
 PR 25-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 26-JUN-1998; 98US-0090863.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 01-JUL-1998; 98US-0091544.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 07-JUL-1998; 98US-0091978.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 04-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
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 PR 18-AUG-1998; 98US-0096959.
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 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 31-AUG-1998; 98US-0098014.
 PR 16-SEP-1998; 98US-0098525.
 PR 12-JAN-1999; 98US-0100634.
 PR 99US-0115565.
 (GETH) GENENTECH INC.
 PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX MPI; 2000-072883/06.
 DR N-PSDB; AA265023.

XX Membrane-bound proteins and related nucleotide sequences
 PT Claim 12; Fig 139; 822pp; English.
 XX
 PS The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 SQ Sequence 185 AA;
 Query Match 97.7%; Score 216; DB 21; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KKTCTVHKMKKEVMPSTIOSLALVKEKKLOGKPGGPPKGL 42
 DB 78 KKTCTVHKMKKEVMPSTIOSLALVKEKKLOGKPGGPPKGL 119
 RESULT 5
 AAB65209
 ID AAB65209 standard; Protein: 185 AA.
 XX
 AC AAB65209;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
 XX
 KW Human, secreted and transmembrane protein; PRO; cytosolic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000MO-US08439.
 XX
 PR 02-JUN-1999; 99MO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30911.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US00365.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.

24-FEB-2000: 2000WO-US05004.
PR 02-MAR-2000: 2000WO-US05841.
PR 15-MAR-2000: 2000WO-US06884.
PR 20-MAR-2000: 2000WO-US07377.
XX
XX
PA (GENTH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
XX
DR WPI: 2001-032160/04.
DR N-PSDB: AAF44169.
XX
XX
PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
XX
PS Claim 12: Fig 139; 935pp; English.
XX
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes. In
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX
SQ Sequence 185 AA;
XX
XX
Query Match 97.7%; Score 216; DB 22; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKTCTVHKMKKEVMPSTIOSDALVKEKKLOGKPGGPPKGL 42
Db 78 KKTCTVHKMKKEVMPSTIOSDALVKEKKLOGKPGGPPKGL 119
XX
XX
RESULT 6
AAB50957
ID AAB50957 standard; Protein: 185 AA.
XX
XX
AC AAB50957;
XX
XX
DT 21-MAR-2001 (first entry)
XX
XX
DE Human PRO1005 protein.
XX
XX
KW Human; PRO: cytostatic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200073348-A2.
XX
XX
PD 07-DEC-2000.
XX
XX
PF 30-MAY-2000: 2000WO-US14941.
XX
XX
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-0140650.
PR 23-JUN-1999; 99US-0141037.

20-JUL-1999; 99US-0144758.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US30095.
PR 16-DEC-1999; 99WO-US30995.
PR 20-DEC-1999; 99WO-US30999.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-0187202.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
XX
XX
PA (GENTH) GENENTECH INC.
XX
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
XX
DR WPI: 2001-016509/02.
DR N-PSDB: AAC91559.
XX
XX
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT for treating various tumors, e.g. breast cancer, and other
PT inflammatory, angiogenic and immunological disorders -
XX
XX
PS Claim 31: Fig 14; 188pp; English.
XX
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumors, e.g.,
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC central nervous system cancer, melanoma or leukaemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytic,
CC hypothalamic and other glandular, macropapillary, epithelial, stromal and
CC blastocoele disorders, and inflammatory, angiogenic and immunological
CC disorders.
XX
XX
SQ Sequence 185 AA;
XX
XX
Query Match 97.7%; Score 216; DB 22; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKTCTVHKMKKEVMPSTIOSDALVKEKKLOGKPGGPPKGL 42
Db 78 KKTCTVHKMKKEVMPSTIOSDALVKEKKLOGKPGGPPKGL 119
XX
XX
RESULT 7
AAB95492
ID AAB95492 standard; Protein: 185 AA.
XX
XX
AC AAB95492;
XX
XX
DT 19-JUL-2002 (first entry)
XX
XX
DE Human angiogenesis related protein PRO1005 SEQ ID NO: 140.
XX
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardant; cytostatic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic.
XX
XX
OS Homo sapiens.
XX
XX

PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23338.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30873.
 PR 10-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERR/) GERBER H.
 PA (GERR/) GERRTSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95630.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 140; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.
 XX
 SQ Sequence 185 AA;
 Query Match 97.7%; Score 216; DB 23; Length 185;
 Best local Similarity 97.6%; Pred. No. 2.4e-19;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLGKGGPPKGL 42
 DB 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLGKGGPPKGL 119
 RESULT 8
 ABB84886
 ID ABB84886 standard; Protein; 185 AA.
 XX
 AC ABB84886;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO1005 protein sequence SEQ ID NO:140.
 XX
 KW Human; angiogenesis; cardiatic; cytoslastic; antiangiogenic; hypotensive;
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial stenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23338.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.

PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001US-087092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001US-0871743.
 PR 01-JUN-2001; 2001US-08717800.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-090516/12.
 DR N-PSDB: ABL88141.
 DR
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11: Fig 140; 565pp: English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 185 AA;
 Query Match 97.7%; Score 216; DB 23; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KKTCTVHKMKKEVMPISIOSDALVKEKKLOGKPGGPPKGL 42
 DB 78 KKTCTVHKMKKEVMPISIOSDALVKEKKLOGKPGGPPKGL 119
 RESULT 9
 AAB83665
 ID AAB83665 standard; Protein; 185 AA.
 AC AAB83665;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 148.
 XX
 DE Human PRO protein, Seq ID No 148.
 XX
 KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX

PF 29-JUN-2001; 2001US-0821066.
 XX
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000US-220710.
 PR 23-AUG-2000; 2000US-220710.
 PR 24-AUG-2000; 2000US-220710.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000US-0530873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000US-053678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0506520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0854280.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gertlisen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-172001/22.
 DR N-PSDB: ABB33609.
 DR
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours,
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11: Figure 148; 359pp: English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAB83592-AAB83713 represent human PRO
 CC protein sequences of the invention.
 CC
 XX
 SQ Sequence 185 AA;
 Query Match 97.7%; Score 216; DB 23; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.4e-19;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 KKTCTVHKMKKEVMPISIOSDALVKEKKLOGKPGGPPKGL 42
 DB 78 KKTCTVHKMKKEVMPISIOSDALVKEKKLOGKPGGPPKGL 119
 RESULT 10
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 AC AAB38329;
 XX
 PD 31-JAN-2002.
 XX

DT 31-JAN-2001 (first entry)
XX Human secreted protein encoded by gene 9 clone HNSAD53.
XX
XX Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
XX cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
XX neurotropic; antibacterial; virucide; fungicide; ophthalmological; human;
XX vulnerable; gene therapy; infection; secreted protein.
XX
XX Homo sapiens.
XX
XX WO200061623-A1.
XX
XX 19-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US08979.
XX
XX 09-APR-1999; 99US-0128693.
XX 26-APR-1999; 99US-0130991.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
XX Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
XX Young PE;
XX
XX WPI: 2000-647418/62.
XX
XX New nucleic acid molecules encoding 62 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives -
XX
XX Claim 11; Page 598; 716pp; English.
XX
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
XX human secreted proteins encoded by the genes AAC69512-C69587. The genes
XX and proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated from
XX a range of human tissues disclosed in the specification. The nucleic
XX acids, proteins, antibodies and (ant)agonists are useful in the
XX diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
XX rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
XX of the breast or liver; (c) cardiovascular disorders e.g. cardiac
XX arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
XX angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
XX infections caused by bacteria, viruses and fungi; and (h) ocular
XX disorders e.g. corneal infection. The polypeptides can also be used to
XX aid wound healing and epithelial cell proliferation, to prevent skin
XX aging due to sunburn, to maintain organs before transplantation, for
XX supporting cell culture of primary tissues, to regenerate tissues and in
XX chemotaxis.
XX
XX Sequence 186 AA:
SO
Query Match 97.7%; Score 216; DB 21; Length 186;
Best Local Similarity 97.6%; Pred. No. 2.4e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 42
Db 78 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 119
RESULT 11
AAW69974
ID AAW69974 standard; Protein; 194 AA.
XX
XX AAW69974;
XX
XX 16-NOV-1998 (first entry)
XX
XX Cancer associated protein.
XX

KW Cancer; PCR; Northern blotting; ribonuclease protection assay;
KW diagnosis; metastatic cancer.
XX
XX Synthetic.
XX
XX WO9837187-A1.
XX
XX 27-AUG-1998.
XX
XX 18-FEB-1998; 98MO-JP00667.
XX
XX 21-FEB-1997; 97JP-0052508.
XX
XX (TAKI) TAKARA SHUZO CO LTD.
XX
XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
XX
XX WPI: 1998-467552/40.
XX
XX Detection of cancer cells in tissue samples - by changes in mRNA
XX expression compared to normal tissue of specific cancer-associated
XX gene sequences
XX
XX Claim 14; Page 64-65; 92pp; Japanese.
XX
XX The cancer associated proteins AAW69974-W69976 where used in the method
XX of the invention to detect cancer cells in tissue samples or biological
XX fluids. They are detected by monitoring the change in mRNA expression
XX as compared to normal tissue of one or more cancer-associated genes
XX whose cDNA stringently hybridises to cancer associated gene nucleic acid
XX fragments. The change in expression may be an increase or a decrease
XX compared to normal tissue. The mRNA expression may be determined by
XX PCR, Northern blotting or ribonuclease protection assay, or by
XX determining the change in the amount of protein encoded by the gene(s) as
XX compared to normal tissue, for example by using a labelled antibody
XX recognising the protein. Detection of cancer cells for cancer diagnosis,
XX including detection of metastatic cancer cells in tissues other than the
XX primary tumour site.
XX
XX Sequence 194 AA:
SO
Query Match 97.7%; Score 216; DB 19; Length 194;
Best Local Similarity 97.6%; Pred. No. 2.5e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 42
Db 87 KKTCTVHKMKKEVMPISQSLDALVKEKKIQGKGPGGPPPKGL 128
RESULT 12
AAW76591
ID AAW76591 standard; Protein; 194 AA.
XX
XX AAW76591;
XX
XX 10-APR-2000 (first entry)
XX
XX Human ovarian tumor EST fragment encoded protein 87.
XX
XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;
XX gene therapy; treatment.
XX
XX Homo sapiens.
XX
XX DE19817557-A1.
XX
XX 21-OCT-1999.
XX
XX 09-APR-1998; 98DE-1017557.
XX
XX 09-APR-1998; 98DE-1017557.
XX
XX 09-APR-1998; 98DE-1017557.
XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX WPI: 1999-591920/51.
XX N-PSDB: AAZ77487.
XX
XX New nucleic acid sequences expressed in ovarian, and some other, cancer
PT tissues, and derived polypeptides, for treatment of ovarian cancer and
PT identification of therapeutic agents -
XX
PS Claim 25; Page 279; 310pp; German.
XX
XX This invention describes novel nucleic acid (cDNA) sequences (A) which
CC have anticancer activity and are highly expressed in ovarian tumor
CC tissue (and some also in testis and breast cancer tissue). The products
CC of the invention can be used for gene therapy. (A) are used (1) for
CC recombinant expression of polypeptides (B) and (1) to isolate complete
CC genes. (B) are used (1) to identify agents suitable for treatment of
CC ovarian cancer; (11) directly for treating this form of cancer
CC (including expression from gene therapy vectors) and (11) for generation
CC of specific antibodies. (A) are identified by assembling ESTs (expressed
CC sequence tags) from a particular tissue type before comparison of
CC expression patterns. This allows a significantly longer fragment of the
CC gene to be revealed, so should reduce the number of failures associated
CC with the fact that ESTs from different libraries may represent different
CC parts of the same unknown gene, distorting the estimated frequency of
CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
CC fragments encoded by the human ovarian tumor cDNA library derived EST
CC fragments represented in AAZ77450-777572.
XX
SO Sequence 194 AA:
XX
XX Query Match 97.7%; Score 216; DB 20; Length 194;
XX Best Local Similarity 97.6%; Pred. No. 2.5e-19;
XX Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 KKTCTVHKMKKEVMPISQSDALVKEKKLOGKGGPPKGL 42
DB 87 KKTCTVHKMKKEVMPISQSDALVKEKKLOGKGGPPKGL 128
RESULT 13
ABP09922
ID ABP09922 standard; Protein; 184 AA.
XX
XX AC ABP09922;
XX
XX 24-JUN-2002 (first entry)
DE
XX
XX Human ORFX protein sequence SEQ ID NO:19826.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KM hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;
KM degenerative disorder; osteoarthritis; neurodegenerative disorder;
KM cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KM hypertension; hypothyroidism; cholesterol ester storage disease;
KM immune deficiency; immune disorder; infectious disease;
KM autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KM myasthenia gravis.
XX
XX Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
PD
XX
XX 29-MAY-2001; 2001WO-0510836.
PF
XX
XX 30-MAY-2000; 2000US-206132P.
PR
XX 29-AUG-2000; 2000US-228716P.
XX
XX (CURA-) CURAGEN CORP.
PA

XX
XX Shimkels RA, Leach MD;
XX
XX WPI: 2002-106308/14.
XX
XX N-PSDB: ABN25674.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -
XX
PS Disclosure; SEQ ID 19826; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SO Sequence 184 AA:
XX
XX Query Match 62.0%; Score 137; DB 23; Length 184;
XX Best Local Similarity 64.3%; Pred. No. 2.1e-09;
XX Matches 27; Conservative 5; Mismatches 8; Indels 2; Gaps 1;
OY 1 KKTCTVHKMKKEVMPISQSDALVKEKKLOGKGGPPKGL 42
DB 78 KKTCTVHKMKKEVMPISQSDALVKEKKLOGKGGPPKGL 117
RESULT 14
AAB41048
ID AAB41048 standard; Protein; 103 AA.
XX
XX AC AAB41048;
XX
XX 08-FEB-2001 (first entry)
DE
XX
XX Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.
XX
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KM vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KM anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KM antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive.

Best Local Similarity 37.88; Pred. No. 2.8;
 Matches 14; Conservative 7; Mismatches 15; Indels 1;
 Gaps 1;
 QY 4 CIVHKKKEVMPISQSLDALVKEKKLOGKPGGPPPK 40
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 Db 39 CLGAKHKAQSL-QLSLADSPFLKLRKSSGKPGNPRPK 74

Search completed: April 11, 2003, 16:11:11
 Job time : 12.7847 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 ; Search time 4.17945 Seconds
(without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726a-13_COPY_78_119

Perfect score: 221
Sequence: 1 KKTCTVHKMKKEVMPSTQSL.....LVKREKLLQGGPGGPPPKGL 42

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/ptodata/2/pubppaa/PC7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/2/pubppaa/PC7US_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	97.7	182	US-10-050-704-212	Sequence 212, App
2	216	97.7	185	US-09-992-598-211	Sequence 211, App
3	216	97.7	185	US-09-989-293A-211	Sequence 211, App
4	216	97.7	185	US-09-989-735-211	Sequence 211, App
5	216	97.7	185	US-09-990-444-211	Sequence 211, App
6	216	97.7	185	US-10-001-054-14	Sequence 14, App
7	216	97.7	185	US-09-989-730-211	Sequence 211, App
8	216	97.7	185	US-09-990-436-211	Sequence 211, App
9	216	97.7	185	US-09-991-181-211	Sequence 211, App
10	216	97.7	185	US-09-993-687-211	Sequence 211, App
11	216	97.7	185	US-09-989-734-211	Sequence 211, App
12	216	97.7	185	US-09-997-653-211	Sequence 211, App
13	216	97.7	185	US-09-993-667-211	Sequence 211, App
14	216	97.7	185	US-09-990-438-211	Sequence 211, App
15	216	97.7	185	US-09-990-562-211	Sequence 211, App
16	216	97.7	185	US-09-997-428-211	Sequence 211, App
17	216	97.7	185	US-09-997-666-211	Sequence 211, App
18	216	97.7	185	US-10-227-884-148	Sequence 148, App
19	216	97.7	185	US-09-990-711-211	Sequence 211, App

20	216	97.7	185	US-10-230-163-148	Sequence 148, App
21	216	97.7	185	US-09-989-726-211	Sequence 211, App
22	216	97.7	185	US-09-746-763-146	Sequence 146, App
23	216	97.7	185	US-09-990-437-211	Sequence 211, App
24	216	97.7	185	US-09-998-156-211	Sequence 211, App
25	216	97.7	185	US-10-218-631-148	Sequence 148, App
26	216	97.7	185	US-10-230-338-148	Sequence 148, App
27	216	97.7	185	US-09-991-157-211	Sequence 211, App
28	216	97.7	185	US-09-991-172-211	Sequence 211, App
29	216	97.7	185	US-09-997-514-211	Sequence 211, App
30	216	97.7	185	US-09-997-573-211	Sequence 211, App
31	216	97.7	185	US-10-050-704-105	Sequence 105, App
32	216	97.7	185	US-10-230-414-148	Sequence 148, App
33	216	97.7	185	US-09-990-443-211	Sequence 211, App
34	216	97.7	185	US-09-990-726-211	Sequence 211, App
35	216	97.7	185	US-09-997-559-211	Sequence 211, App
36	216	97.7	185	US-09-997-601-211	Sequence 211, App
37	216	97.7	185	US-09-989-729A-211	Sequence 211, App
38	216	97.7	185	US-09-990-440-211	Sequence 211, App
39	216	97.7	185	US-09-991-854-211	Sequence 211, App
40	216	97.7	185	US-09-997-349-211	Sequence 211, App
41	216	97.7	185	US-09-997-440-211	Sequence 211, App
42	216	97.7	185	US-09-997-628-211	Sequence 211, App
43	216	97.7	185	US-09-997-683-211	Sequence 211, App
44	216	97.7	185	US-09-989-722-211	Sequence 211, App
45	216	97.7	185	US-09-989-723-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-10-050-704-212
; Sequence 212, Application US/10050704
; Publication No. US2003050442A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-050-704-212

Query Match 97.7%; Score 216; DB 9; Length 182;
Best Local Similarity 97.6%; Pred. No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTQSLDALVKEKKLQGGPGGPPPKGL 42
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Db 78 KKTCTVHKMKKEVMPSTQSLDALVKEKKLQGGPGGPPPKGL 119

RESULT 2
US-09-992-598-211
; Sequence 211, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashtkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC20
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1997-11-24
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 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEMWPSIOSLALVYKREKLOGKGGPPKGL 42
Db 78 KKTCTVHKMKKEMWPSIOSLALVYKREKLOGKGGPPKGL 119

RESULT 3
US-09-989-293A-211
Sequence 211, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Askenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavina, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C66
CURRENT FILING DATE: 2001-11-20
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
Best local Similarity 97.6%; Pred. No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKKEVMPSTQSLDALVKEKKLOGKGGPPPKGL 42
DB 78 KKTCTVHKKEVMPSTQSLDALVKEKKLOGKGGPPPKGL 119

RESULT 4
US-09-989-735-211
;; Sequence 211, Application US/09989735
;; Publication No. US20020193299A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Destroyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TIME OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P27301C61
 CURRENT APPLICATION NUMBER: US/09/989,735
 PRIOR APPLICATION NUMBER: 2001-11-19
 PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 78 KKTCTVHKMKKEVMPSTOSLDALVEKKLGKGGPGPPKGL 42
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RESULT 5
 US-09-980-444-211
 Sequence 211, Application US/09990444
 Publication No. US20020193300A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botsstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey J.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Scewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C19
 CURRENT APPLICATION NUMBER: US/09/990,444
 PRIOR FILING DATE: 2001-11-14
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTQSLDLVKEKKLOGKGGPPPKGL 42
 DB 78 KKTCTVHKMKKEVMPSTQSLDLVKEKKLOGKGGPPPKGL 119

RESULT 6
 US-10-001-054-14
 Sequence 14, Application US/10001054
 Publication No. US20020192209A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Baker, Kevin
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin
 APPLICANT: Hebert, Carolyn
 APPLICANT: Henzel, William
 APPLICANT: Kabakoff, Rhona
 APPLICANT: Shelton, David
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin
 APPLICANT: Wood, William
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC
 FILE REFERENCE: P3034R1PCT
 CURRENT APPLICATION NUMBER: US/10/001, 054
 CURRENT FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 60/059114
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 14
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-001-054-14

Query Match 97.7%; Score 216; DB 9; Length 185;
Best Local Similarity 97.6%; Pred. No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKRVMSIOSLDALVKEKRIQGGKGGPPPKGL 42
DB 78 KKTCTVHKMKKRVMSIOSLDALVKEKRIQGGKGGPPPKGL 119

RESULT 7
US-09-989-730-211
Sequence 211, Application US/09989730
Publication No. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-07-09

Query Match 97.7% Score 216; DB 9; Length 185;
Best Local Similarity 97.6% Pred No. 2.5e-20;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Sequence 211, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kijavrin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990.436
PRIOR FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-05-07

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Query Match Best Local Similarity 97.7%; Score 216; DB 9; Length 185;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9
 US-09-991-181-211

;; Sequence 211, Application US/09991181
 ;; Publication No. US20020197615A1
 ;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
 ;; APPLICANT: Baker, Kevin P.
 ;; APPLICANT: Bolstein, David
 ;; APPLICANT: Desnoyers, Luc
 ;; APPLICANT: Eaton, Dan L.
 ;; APPLICANT: Ferrara, Napoleone
 ;; APPLICANT: Fong, Sherman
 ;; APPLICANT: Gerber, Hanspeter
 ;; APPLICANT: Gerritsen, Maty E.
 ;; APPLICANT: Goddard, Audrey
 ;; APPLICANT: Godowski, Paul J.
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 ;; APPLICANT: Paoni, Nicholas F.
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 ;; APPLICANT: Stewart, Timothy A.
 ;; APPLICANT: Tumas, Daniel
 ;; APPLICANT: Watanabe, Colin K.
 ;; APPLICANT: Williams, P. Mickey
 ;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ;; TITLE OF INVENTION: Acids Encoding the Same
 ;; FILE REFERENCE: P2730P1C53

;; CURRENT APPLICATION NUMBER: US/09/991,181

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 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best local similarity 97.6%; Pred. No. 2,35e-20;

Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKKEVMPSTQSLDALVKEKRIQGGPGGPPKGL 42
 Db 78 KKTCTVHKMKKEVMPSTQSLDALVKEKRIQGGPGGPPKGL 119

RESULT 10
 US-09-993-687-211
 ; Sequence 211, Application US/09993687
 ; Publication No. US20020198149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botsstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gertlisen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Guiney, Austin L.
 ; APPLICANT: Kijavits, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C11
 ; CURRENT APPLICATION NUMBER: US/09/993,687
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best local Similarity 97.6%; Pred. No. 2.5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCIVHKKKEVMPSTQSIDALVKEKKLOGKGGPPPKGL 42
 DB 78 KTCIVHKKKEVMPSTQSIDALVKEKKLOGKGGPPPKGL 119

RESULT 11
US-09-989-734-211
Sequence 211, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Genber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Nepier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 97.7%; Score 216; DB 9; Length 185;

Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMSISLDAVYKKKLGKGGGPPPKGL 42
Db 78 KKTCTVHKMKKEVMSISLDAVYKKKLGKGGGPPPKGL 119

RESULT 12
US-09-997-653-211

; Sequence 211, Application US/09997653

; Publication No. US20030008297A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2,5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTIOSDALVREKRIQGGKPGGPPKGL 42
 DB 78 KKTCTVHKMKKEVMPSTIOSDALVREKRIQGGKPGGPPKGL 119

RESULT 13
 US-09-993-667-211
 Sequence 211, Application US/09993667
 Publication No. US20030022187A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993.667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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 ? PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2,5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVWPSTQSDALVKEKKLOGKGGPPPKGL 42
 DB 78 KKTCTVHKMKKEVWPSTQSDALVKEKKLOGKGGPPPKGL 119

RESULT 14
 US-09-990-438-211

? Sequence 211, Application US/09990438
 ? Publication No. US20030027754A1
 ? GENERAL INFORMATION:

? APPLICANT: Ashkenazi, Avi J.
 ? APPLICANT: Baker, Kevin P.
 ? APPLICANT: Bolstein, David
 ? APPLICANT: Desnoyers, Luc
 ? APPLICANT: Eaton, Dan L.
 ? APPLICANT: Ferrara, Napoleone
 ? APPLICANT: Fong, Sherman
 ? APPLICANT: Gerber, Hanspeter
 ? APPLICANT: Gertlisen, Mary E.
 ? APPLICANT: Goddard, Audrey
 ? APPLICANT: Godowski, Paul J.
 ? APPLICANT: Grimaldi, J. Christopher
 ? APPLICANT: Gurney, Austin L.
 ? APPLICANT: Kljavin, Ivar J.
 ? APPLICANT: Napier, Mary A.
 ? APPLICANT: Pan, James

? APPLICANT: Paoni, Nicholas F.
 ? APPLICANT: Roy, Margaret Ann
 ? APPLICANT: Stewart, Timothy A.
 ? APPLICANT: Tumas, Daniel
 ? APPLICANT: Watanabe, Colin K.
 ? APPLICANT: Williams, P. Mickey
 ? APPLICANT: Wood, William I.
 ? APPLICANT: Zhang, Zemin
 ? TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
 ? FILE OF INVENTION: Acids Encoding the Same
 ? FILE REFERENCE: P2730P1C3
 ? CURRENT APPLICATION NUMBER: US/09/990,438
 ? CURRENT FILING DATE: 2001-11-14
 ? PRIOR APPLICATION NUMBER: 60/049787
 ? PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
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 PRIOR APPLICATION NUMBER: 60/091626
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 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKKEVMPSTQSLDALVKKTKGSGGPPPKGL 42
 DB 78 KKTCTVHKMKKEVMPSTQSLDALVKKTKGSGGPPPKGL 119

RESULT 15
 US-09-990-562-211
 Sequence 211, Application US/09990562
 Publication No. US20030027985A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey J.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C18
CURRENT APPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 97.7%; Score 216; DB 9; Length 185;
 Best Local Similarity 97.6%; Pred. No. 2.5e-20;
 Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KTCIVHKMKKEVMSIOSLDAVKEKKGKGGPPPKGL 42
 Db 78 KTCIVHKMKKEVMSIOSLDAVKEKKGKGGPPPKGL 119

Search completed: April 11, 2003, 16:17:44
 Job time : 5.17945 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 2.46656 Seconds
(Without alignments)
706.250 Million cell updates/sec

Title: US-09-821-726a-13_COPY_78_119
Perfect score: 221
Sequence: 1 KKTCTVHKMKRKYVPSIQSLDYLVEKKLQKGGPPPKGL 42

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	216	97.7	199	1	CLIP_HUMAN
2	151	68.3	184	1	CLIP_MOUSE
3	59.5	26.9	682	1	KPCG_BOVIN
4	59.5	26.9	697	1	KPCG_HUMAN
5	59.5	26.9	697	1	KPCG_MOUSE
6	59.5	26.9	697	1	KPCG_RABIT
7	59	26.7	759	1	TOP3_CAEEL
8	57.5	26.0	634	1	FTSH_AQUAE
9	57.5	26.0	2469	1	TECU_HSVSA
10	57	25.8	997	1	PRO_SORFI
11	55	24.9	230	1	DCTR_BACHD
12	55	24.9	431	1	PXR_MOUSE
13	55	24.9	431	1	PXR_RAT
14	54.5	24.7	477	1	FES_FSVST
15	54.5	24.7	820	1	FES_FELCA
16	54	24.4	875	1	GYRA_ECOLI
17	54	24.4	876	1	GYRA_KLEPN
18	53.5	24.2	542	1	CPA3_RAT
19	53.5	24.2	542	1	TUL1_HUMAN
20	53.5	24.2	2144	1	CLR2_MOUSE
21	53.5	24.2	2920	1	CLR2_MOUSE
22	53	24.0	233	1	HB2A_RAT
23	53	24.0	263	1	HB2B_RAT
24	53	24.0	695	1	DVL1_MOUSE
25	53	24.0	695	1	DVL1_RAT
26	52.5	23.8	303	1	PYP3_SCHPO
27	52.5	23.8	648	1	WHN_HUMAN
28	52.5	23.8	1189	1	YJH6_YEAST
29	52	23.5	252	1	HB2F_MOUSE
30	52	23.5	263	1	HB2K_MOUSE
31	52	23.5	263	1	HB2L_MOUSE
32	52	23.5	263	1	HB2U_MOUSE
33	52	23.5	265	1	HB2A_MOUSE

34	52	23.5	265	1	HB2D_MOUSE	P01921 mus musculus
35	52	23.5	265	1	HB2Q_MOUSE	P06342 mus musculus
36	52	23.5	268	1	HB2Q_HUMAN	P05338 homo sapien
37	52	23.5	494	1	CPA4_MOUSE	P15392 mus musculus
38	52	23.5	494	1	CPA5_MOUSE	P20852 mus musculus
39	52	23.5	878	1	GYRA_ERWCA	P41513 erwinia car
40	51.5	23.3	434	1	PXR_HUMAN	O75469 homo sapien
41	51.5	23.3	656	1	HS7C_DROME	P29844 drosophila
42	51.5	23.3	928	1	DNL1_CANAL	P52496 candida alb
43	51	23.1	282	1	YHP0_YEAST	P38806 saccharomyc
44	51	23.1	333	1	PTX2_CHICK	O93385 gallus gall
45	51	23.1	379	1	Y67L_CHLMO	O9pk02 chlamydia m

ALIGNMENTS

RESULT 1
ID CLIP_HUMAN STANDARD: PRT; 199 AA.

AC Q9NS71:
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)

DE CA11 protein.

GN CA11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;

RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;

RT Isolation of two novel genes, down-regulated in gastric cancer.;

RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is

CC detected in cancer tissue or gastric cancer cell lines.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).

CC EMBL: AB039886; BAA92433.1; -
DR MIM: 606402; -
SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A138D7A CRC64;

Query Match 97.7%; Score 216; DB 1; Length 199;
Best Local Similarity 97.6%; Pred. No. 5e-19;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKRKYVPSIQSLDYLVEKKLQKGGPPPKGL 42
DB 92 KKTCTVHKMKRKYVPSIQSLDYLVEKKLQKGGPPPKGL 133

RESULT 2
ID CLIP_MOUSE STANDARD: PRT; 184 AA.

AC Q9CR36; Q9D7R7; Q9CR25;

DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE CA11 protein homolog.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Saito K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schiml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 Hayashizaki Y.;
 RA Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -----
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 CC -----
 DR EMBL: AK008990; BAB26010.1;
 DR EMBL: AK008622; BAB25784.1;
 DR EMBL: AK008641; BAB25801.1;
 DR EMBL: AK008647; BAB25805.1;
 DR EMBL: AK008722; BAB25856.1;
 DR EMBL: AK008745; BAB25872.1;
 DR EMBL: AK008933; BAB25975.1;
 DR EMBL: AK008956; BAB25988.1;
 DR EMBL: AK009145; BAB26103.1;
 DR EMBL: AK019050; BAB31525.1;
 DR MGD: MGI:193533; 220002K2R1K.
 FT CONFLICT 113 113 P -> L (IN REF. 1: BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288962F0404FFRAB CRC64;
 Query Match 68.3%; Score 151; DB 1; Length 184;
 Best Local Similarity 66.7%; Pred. No. 3e-11;
 Matches 28; Conservative 6; Mismatches 6; Indels 2; Gaps 1;
 OY 1 KKTCTVHKMKKEVPSQSLSQSDATVKEKKLGKGGGPPPKGL 42
 DB 78 KKSCIVHRMKDAMPISLQDDPTMYKEOK--GKGPGGAPKDL 117
 RESULT 3
 KPGC_BOVIN STANDARD; PRT; 682 AA.
 AC P05128;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C, gamma type (EC 2.7.1.1-) (PKC-gamma) (Fragment).
 GN PRCG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

MEDLINE=86289426; PubMed=3755548;
 RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
 RA Waterfield M.D., Franke U., Ullrich A.;
 RT Multiple, distinct forms of bovine and human protein kinase C
 RT suggest diversity in cellular signaling pathways.";
 RL Science 233:855-866(1986).
 RN [2]
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=3045562;
 RA Nishizuka Y.;
 RT "The molecular heterogeneity of protein kinase C and its implications
 RT for cellular regulation.";
 RL Nature 334:661-665(1988).
 CC -----
 CC FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
 CC BINDING DOMAINS: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M13976; AAA30704.1;
 DR PIR: C24664; KIRGCG.
 DR HSSP: P05697; ITBN.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000961; Pkinase.C.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR Pfam: PF00130; DAG_PE-bind.2.
 DR Pfam: PF00168; C2.1.
 DR Pfam: PF00433; Pkinase.C.1.
 DR ProDom: PD000001; Euk_Pkinase.1.
 DR SMART: SM00109; C1; 2.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00133; S_TK_X.1.
 DR SMART: SM00220; S_TK_X.1.
 DR PROSITE: PS00499; C2_DOMAIN.1; 1.
 DR PROSITE: PS00499; C2_DOMAIN.2; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM.1; 2.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM.2; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM.1.
 DR Calcium-binding; Repeat: ATP-binding; Transferase;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW Phosphorylation.
 FT NON_TER 1
 FT DOMAIN 21 70 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 155 245 C2 DOMAIN.
 FT DOMAIN 336 599 PROTEIN KINASE.
 FT NP_BIND 342 350 ATP (BY SIMILARITY).
 FT BINDING 365 365 ATP (BY SIMILARITY).
 FT ACT_SITE 465 465 BY SIMILARITY.
 FT MOD_RES 633 633 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 640 640 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 682 AA; 77156 MW; 20392D11188C731C CRC64;
 Query Match 26.9%; Score 59.5; DB 1; Length 682;
 Best Local Similarity 39.4%; Pred. No. 12;

Matches	1;	Conservative	7;	Mismatches	10;	Indels	3;	Gaps	1;
Qy	9	MKEKMEPSIQSLALVKEK	---	LQKGGPGGP	38				
Db	367	LKDDIVODDDVDCTLVEKRYIALGGRRGPGGR	399						
RESULT 4									
KPCG_HUMAN		STANDARD;	PRT;	697	AA.				
ID	KPCG_HUMAN								
AC	P05129;								
DT	13-AUG-1987 (Rel. 05, Created)								
DT	01-FEB-1994 (Rel. 28, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	Protein Kinase C, gamma type (EC 2.7.1.-) (PKC-gamma).								
OS	PKCγ OR PKCγ.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxId=9606;								
LN	111								
RP	SEQUENCE FROM N.A.								
RA	Cui W.C., Yu L., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;								
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.								
RN	[2]								
RP	SEQUENCE OF 1-318 FROM N.A.								
RC	TISSUE=Brain;								
RX	MEDLINE=86289426; PubMed=3755548;								
RA	Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,								
RA	Waterfield M.D., Francke U., Ullrich A.;								
RT	"Multiple, distinct forms of bovine and human protein kinase C								
RT	suggest diversity in cellular signaling pathways.";								
RL	Science 233:859-866(1986).								
RN	[3]								
RP	SEQUENCE OF 162-697 FROM N.A.								
RC	TISSUE=Hippocampus;								
RA	MEDLINE=93587312; PubMed=8375396;								
RA	Kochs G., Meyer D., Hug H., Merme D., Sarre T.F.;								
RT	"Activation and substrate specificity of the human protein kinase C								
RT	alpha and zeta isoenzymes.";								
RL	Eur. J. Biochem. 216:597-606(1993).								
RN	[4]								
RP	VARIANTS C-141: Q-415, D-523 AND S-659.								
RA	MEDLINE=98213587; PubMed=9545390;								
RA	Al-Maghitthen M., Vithana E.N., Inglehearn C.F., Moore T., Bird A.C.,								
RA	Bhattacharya S.S.;								
RT	"Segregation of a PKCγ mutation in two RP11 families.";								
RL	Am. J. Hum. Genet. 62:1248-1252(1998).								
RN	[5]								
RP	SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RP11.								
RA	MEDLINE=99375047; PubMed=10441600;								
RA	Dryja T.P., McEvoy J., McGee T.L., Berson E.L.;								
RT	"No mutations in the coding region of the PKCγ gene in three families								
RT	with retinitis pigmentosa linked to the RP11 locus on chromosome								
RT	19q.";								
RL	Am. J. Hum. Genet. 65:926-928(1999).								
CC	-1- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,								
CC	SERINE- AND THREONINE-SPECIFIC ENZYME.								
CC	-1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN								
CC	PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS								
CC	THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.								
CC	-1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG								
CC	BINDING DOMAINS.								
CC	-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.								
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.								
CC	PKC SUBFAMILY.								
CC	-1- DATABASE: NAME=Mutations of the PKCγ gene;								
CC	NOTE=Retina International's Scientific Newsletter;								
CC									

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CC	-----
DR	EMBL; AF345987; AAK13533.1; -
DR	EMBL; M13977; AAA60102.1; ALT_TERM.
DR	EMBL; Z15114; CAA78820.1; -
DR	PIR; D24664; D24664.
DR	HSSP; P05697; ITBN.
DR	Genew; HGNC:9402; PRKCG.
DR	MIM; 176980; -
DR	InterPro; IPR000008; C2.
DR	InterPro; IPR002219; DAG_PE-bind.
DR	InterPro; IPR000719; Euk_pkinase.
DR	InterPro; IPR000961; pkinase_C.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	pfam; PF00069; pkinase_1.
DR	pfam; PF00130; DAG_PE-bind; 2.
DR	pfam; PF00168; C2; 1.
DR	PRINTS; PF00433; pkinase_C; 1.
DR	PRINTS; PF00360; C2DOMAIN.
DR	PRINTS; PR00008; DACPEDOMAIN.
DR	Prodom; PD000001; Euk_pkinase; 1.
DR	SMART; SM00109; C1; 2.
DR	SMART; SM00238; C2; 1.
DR	SMART; SM00133; S-TK_X; 1.
DR	SMART; SM00220; S-TRC; 1.
DR	PROSITE; PS00499; C2_DOMAIN_1; 1.
DR	PROSITE; PS50004; C2_DOMAIN_2; 1.
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR	PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR	PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	Calcium-binding; Repeat; ATP-binding; Transferase;
KW	Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW	Phosphorylation; Polymorphism
FT	DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT	DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT	DOMAIN 170 260 C2 DOMAIN.
FT	DOMAIN 351 614 PROTEIN KINASE.
FT	NP_BIND 357 365 ATP (BY SIMILARITY).
FT	BINDING 380 380 ATP (BY SIMILARITY).
FT	ACT_SITE 480 480 BY SIMILARITY.
FT	MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	VARIANT 141 141 R -> C.
FT	VARIANT 415 415 /FTID=VAR_008755.
FT	VARIANT 523 523 H -> Q.
FT	VARIANT 523 523 /FTID=VAR_008756.
FT	VARIANT 659 659 A -> D.
FT	VARIANT 659 659 /FTID=VAR_008757.
FT	R -> S.
FT	R -> S.
FT	/FTID=VAR_008758.
FT	SEQUENCE 697 AA; 78447 MW; 3F91B5BEF713C41 CRC64;
OY	9 MKKEVMPSTQSLDAIVKEKK---LCKGPGGGPP 38
DQ	382 LKRDDVIYQDDVDCTLVKRVALLGGRGFGGRP 414
DT	Query Match 26.9%; Score 59.5; DB 1; Length 697;
DT	Best Local Similarity 39.4%; Pred. No. 12;
DT	Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1.
DT	RESULT 5
ID	KPCG_MOUSE STANDARD; PRT; 697 AA.
AC	P05697;
DT	01-NOV-1988 (Rel. 09, Created)
DT	01-JUN-2002 (Rel. 41, Last annotation update)

RL Biochemistry 27:2083-2087(1988).
CC -1- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M19338; AAA31449.1; -
DR PIR: A28708; KIRBGC.
DR HSSP: P05697; ITBN.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR000360; C2DOMAIN.
DR PRINTS: PR000008; DAGPEDOMAIN.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00499; C2 DOMAIN_1; 1.
DR PROSITE: PS00004; C2 DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00017; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Calcium-binding; Repeat: ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 697 AA; 78371 MW; 925D22221F785B5F CRC64;
Query Match 26.9%; Score 59.5; DB 1; Length 697;
Best Local Similarity 39.4%; Pred. No. 12;
Matches 13; Conservative 7; Mismatches 10; Indels 3; Gaps 1;
OY 9 MKKEVMPSTOSLDAIVKEKK---LOGKGFPGPP 38
Db 382 LKKDVIWQDDVDCTLVERKVLALGGGPGGRP 414
RESULT 7
TOP3_CAEEL STANDARD; PRT; 759 AA.
ID TOP3_CAEEL
AC 061660; Q9U223;

DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE DNA topoisomerase III (EC 5.99.1.2).
GN TOP-3 OR Y56A3A.27.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OX [1]
RN SEQUENCE FROM N.A.
RC SPRAIN-Bristol N2;
RA Kim Y.-C., Koo H.-S.;
RT "CDNA cloning and overexpression of Caenorhabditis elegans DNA
RL topoisomerase III.";
RN Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC SPRAIN-Bristol N2;
RA Matthews L.;
RL Submitted (Jan-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN REVISIONS.
RA Durbin R.;
RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF057032; AAC13567.1; -
DR EMBL: AL132860; CAB60518.2; -
DR WormBep: Y56A3A.27; CE28138.
DR InterPro: IPR002936; DNAPrim_toprim.
DR InterPro: IPR003601; DNATopI_ATP_bind.
DR InterPro: IPR003602; DNATopI_DNA_bind.
DR InterPro: IPR000380; ProK_topoisomerase.
DR Pfam: PF01751; Topoisom_bac; 1.
DR PRINTS: PR00417; PRTPISMRASE1.
DR SMART: SM00437; TOP1AC; 1.
DR SMART: SM00436; TOP1BC; 1.
DR SMART: SM00493; TOP1RM; 1.
DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
KW Isomerase; Topoisomerase; DNA-binding.
FT ACT_SITE 334 334 DNA CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 759 AA; 85438 MW; 3D862412D72946BD CRC64;
Query Match 26.7%; Score 59; DB 1; Length 759;
Best Local Similarity 26.2%; Pred. No. 15;
Matches 17; Conservative 7; Mismatches 17; Indels 24; Gaps 2;
OY 1 KKTGIVHKMKKEVMPSTOSLDAIVKEKKLOGKGFPGPP----- 37
Db 566 KEICDGRKQKQEVLDQIGKRAIFVESERRKIGVLSQSLQRYLDKNNQAGGPGGPGGG 625
OY 38 -PPKG 41
Db 626 GPPKG 630
RESULT 8
FTSH_AOUAE STANDARD; PRT; 634 AA.
ID FTSH_AOUAE
AC 067077;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cell division protein ftsH homolog (EC 3.4.24.-).
 GN FTSH OR AQ.936.
 OS Aquifex aeolicus.
 CC Bacteria; Aquificae; Aquificales; Aquificaceae;
 CC Aquifex.
 CC NCBI_TaxID=63363;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 CC -1- FUNCTION: SEEMS TO ACT AS AN ATP-DEPENDENT ZINC METALLOPEPTIDASE
 CC (BY SIMILARITY).
 CC -1- COFACTOR: BINDS 1 ZINC ION (POTENTIAL).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M41.
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 CC EMBL: AEO00714; AAC07029.1; -;
 DR MEROPS: M41.009;
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003959; AAA_ATPase-centr.
 DR InterPro: IPR003960; AAA_sub.
 DR Pfam: PFO00642; Peptidase_M41.
 DR Pfam: PFO0004; AAA_1.
 DR SMART: SM00382; AAA; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRfams: TIGR01241; ftsH_fam; 1.
 DR PROSITE: PS00674; AAA; 1.
 CC Cell division; ATP-binding; Transmembrane; Hydrolase; Metalloprotease;
 KW Zinc; Complete proteome.
 FT DOMAIN 1 5
 FT TRANSMEM 6 26
 FT DOMAIN 27 101
 FT TRANSMEM 102 122
 FT DOMAIN 123 634
 FT NP_BIND 195 202
 FT METAL 418 418
 FT ACT_SITE 419 419
 FT METAL 422 422
 SQ SEQUENCE 634 AA: 70686 MW: 32004635F58A53 CRC64;
 Query Match 26.0%; Score 57.5; DB 1; Length 634;
 Best Local Similarity 40.5%; Pred. No. 19;
 Matches 15; Conservative 7; Mismatches 10; Indels 5; Gaps 1;
 QY 6 VHKMKKEVMPISQSDALVYKKEKKGKGGPPPKGL 42
 Db 160 IEEVKEEYKEITEIYIKDPVKFKL-----GGRPKGV 191
 RESULT 9
 TEGU_HSVSA STANDARD; PRT; 2469 AA.
 AC 001056;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Probable large tegument protein.
 GN 64 OR EERP2.
 OS Herpesvirus saimiri (strain 11).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Rhadinovirus.
 CC NCBI_TaxID=10383;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333688; PubMed=1321287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
 RA Newman C., Wiltmann S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Honess R.W.;
 RT "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC -1- HSV-1 24, EBV BFL1, HVS-1 64, VZV 22, AND HCMV UL48.
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 CC EMBL: X64346; CAA45687.1; -;
 DR EMBL: M86409; AAA46140.1; -;
 DR PIR: H36812; H36812.
 SQ SEQUENCE 2469 AA: 280165 MW: D2B48BDC08644CDB CRC64;
 Query Match 26.0%; Score 57.5; DB 1; Length 2469;
 Best Local Similarity 41.0%; Pred. No. 76;
 Matches 16; Conservative 7; Mismatches 9; Indels 7; Gaps 2;
 QY 5 IVHKMKKEVMPISQSDALVYKKEKKGKGGP---PPK 40
 Db 1122 ILKFEVEVLESYKLN-----KEAKLSLLPNGPVPPTPK 1156
 RESULT 10
 FRO_SORFI STANDARD; PRT; 997 AA.
 AC 009033;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Frequency clock protein.
 GN FRO.
 OS Sordaria fimicola.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariales; Sordariaceae; Sordaria.
 CC NCBI_TaxID=27338;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-FGSC 2918;
 RX MEDLINE=94252311; PubMed=8194516;
 RA Merrow M.W., Dunlap J.C.;
 RT "Intergenic complementation of a circadian rhythmicity defect:
 RT phylogenetic conservation of structure and function of the clock gene
 RT frequency.";
 RL EMBL J. 13:2257-2266(1994).
 CC -1- FUNCTION: CIRCADIAN CLOCK COMPONENT INVOLVED IN THE GENERATION OF
 CC BIOLOGICAL RHYTHMS, IN PARTICULAR IN RHYTHM STABILITY, PERIOD

CC LENGTH, AND TEMPERATURE COMPENSATION. BEHAVES AS A NEGATIVE
CC ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP.
CC - SIMILARITY: BELONGS TO THE PRO FAMILY.
CC -----
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CC -----
CC EMBL: L14467; AAA20825.1; -
CC Biological rhythms; Transcription regulation; Nuclear protein.
CC FT DOMAIN 250 256 POLY-SER.
CC FT DOMAIN 569 573 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 868 894 ASP/GLU-RICH (ACIDIC).
CC SEQUENCE 997 AA; 109056 MW; 2581DD2C62DFF93 CRC64;
SQ
Query Match 25.8%; Score 57; DB 1; Length 997;
Best Local Similarity 32.1%; Pred. No. 34;
Matches 17; Conservative 10; Mismatches 12; Indels 14; Gaps 3;
OY 1 KKTCTIVHKKMK-----EVMPSIOSLD-ALYKEKKLGKGGCPKPKG 41
Db 320 KKKLVARLEQLFTGKISGRNMORIPSDALVSEGTIM--APRPEPEG 370
RESULT 11
DCTR_BACHD STANDARD: PRT; 230 AA.
AC 09K998;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable C4-dicarboxylate response regulator dctr.
GN DCTR OR BH2751.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kihara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331(2000).
CC - FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTR/DCTR.
CC - ESSENTIAL FOR EXPRESSION OF DCTR (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC - PFM: PHOSPHORYLATED BY DCTR (BY SIMILARITY).
CC - SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
CC -----
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CC -----
CC EMBL: AP001516; BAB06470.1; -
CC HSSP: P10957; IRNL.
CC InterPro: IPR001789; Response_reg.
CC Pfam: PF000172; response_reg.1.
CC ProDom: PD000039; Response_reg.1.
CC SMART: SM00448; REC.1.
CC PROSITE: PS00110; RESPONSE_REGULATORY.1.
CC Sensory transduction; Transcription regulation; DNA-binding;
CC Activator; Phosphorylation; Complete proteome.
KW

FT DOMAIN 8 124 RESPONSE REGULATORY.
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT DNA_BIND 183 209 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 230 AA; 26376 MW; 06F065F46FC57D40 CRC64;
Query Match 24.9%; Score 55; DB 1; Length 230;
Best Local Similarity 42.9%; Pred. No. 13;
Matches 15; Conservative 5; Mismatches 13; Indels 2; Gaps 1;
OY 8 KMKKEVMSIOSDALYKEKKLGKGGCPKPKL 42
Db 129 KMKKEAEISQSDLEMITKOKAQAN--MDLPLKGL 161
RESULT 12
PXR_MOUSE STANDARD: PRT; 421 AA.
AC 054915;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Orphan nuclear receptor pXR (Pregnane X receptor).
GN NR112 OR PXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Liver;
RX MEDLINE=98149345; PubMed=9489701;
RA Klierer S.A., Moore J.T., Wade L., Staudinger J.L., Watson M.A.,
RA Jones S.A., McKee D.D., Oliver B.B., Willson T.M., Zetterstrom R.H.,
RA Perlman T., Lehmann J.M.;
RT "An orphan nuclear receptor activated by pregnanes defines a novel
RT steroid signaling pathway."
RL Cell 92:73-82(1998).
CC - FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY
CC PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER.
CC - SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).
CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PXR.1 (SHOWN HERE) AND
CC 2/PXR.2; ARE PRODUCED BY NATURALLY OCCURRING STEROIDS SUCH AS
CC PREGNENOLONE AND PROGESTERONE, SYNTHETIC GLUCOCORTICOIDS AND
CC ANTIGLUCOCORTICOIDS AND 16-ALPHA-CAROTRILE (PCN).
CC - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC NRI SUBFAMILY.
CC -----
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CC -----
CC EMBL: AF031814; AAC39964.1; -
CC HSSP: O75469; IILG.
CC TRANSFAC: T04618; -
CC TRANSFAC: T04619; -
CC MGD: MGI1337040; NR112.
CC InterPro: IPR000536; Hormone_rec_11g.
CC InterPro: IPR001723; Scdhnmu_receptor.
CC InterPro: IPR001628; ZnF_C4steroid.
CC Pfam: PF00104; hormone_rec.1.
CC Pfam: PF00105; zf-C4; 1.
CC PRINTS: PR00047; STROIDOMNER.
CC PRINTS: PR00047; STROIDFINGER.
CC ProDom: PD000035; ZnF_C4steroid.1.
CC SMART: SM00430; HOL1; 1.
CC SMART: SM00399; ZnF_C4; 1.
CC PROSITE: PS00031; NUCLEAR_RECEPTOR.1.
DR

KW Receptor: Transcription regulation; DNA-binding; Nuclear protein;
 FT Zinc-finger; Alternative splicing.
 FT DNA_BIND 38 104 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 38 58 C4-TYPE.
 FT ZN_FING 74 99 C4-TYPE.
 FT DOMAIN 105 201 HINGE.
 FT DOMAIN 202 431 LIGAND-BINDING.
 FT VARSPLIC 171 211 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 431 AA: 49567 MW: F592AF91F689329E CRC64;

Query Match 24.9%; Score 55; DB 1; Length 431;
 Best Local Similarity 34.1%; Pred. No. 25;
 Matches 14; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

OY 2 KTCIVHKKKEVMP---IQSLDALYKER---KLOGKPGG 36
 Db 97 KCLGSGMKKEMIMSDAAYQRRALLIKRKREITEAPPG 137

RESULT 13
 ID PKR_RAT STANDARD; PRT; 431 AA.
 AC O9RIAT;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Orphan nuclear receptor PKR (Pregnane X receptor).
 GN NR112 OR PKR.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=99345883; PubMed=10415106;
 RA Zhang H., Leculysse E., Liu L., Hu M., Matoney L., Zhu W., Yan B.;
 RT "Rat pregnane X receptor: molecular cloning, tissue distribution, and
 Arch. Biochem. Biophys. 368:14-22(1999).
 RT Arch. Biochem. Biophys. 368:14-22(1999).
 CC -1- FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY
 PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER (BY
 SIMILARITY).
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NRI SUBFAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL: AF151377; AAD47214.1; -
 DR HSSP: 075469; IITG.
 DR TRANSFAC: T04629; -
 DR InterPro: IPR000536; Hormone_rec.1.g.
 DR InterPro: IPR001723; Steroid_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; zif-C4.1.
 DR PRINTS: PR00398; STRDHOMNER.
 DR PRINTS: PR00047; STROIDFINGER.
 DR ProDom: PD000035; Znf_C4steroid.1.
 DR SMART: SM00430; HOL1.1.
 DR SMART: SM00398; ZNF_C4.1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR.1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 FT Zinc-finger.
 FT DNA_BIND 38 104 NUCLEAR RECEPTOR-TYPE.

FT ZN_FING 38 58 C4-TYPE.
 FT ZN_FING 74 99 C4-TYPE.
 FT DOMAIN 105 201 HINGE.
 FT DOMAIN 202 431 LIGAND-BINDING.
 SQ SEQUENCE 431 AA: 49660 MW: 4B545F21F9439697 CRC64;

Query Match 24.9%; Score 55; DB 1; Length 431;
 Best Local Similarity 34.1%; Pred. No. 25;
 Matches 14; Conservative 9; Mismatches 12; Indels 6; Gaps 2;

OY 2 KTCIVHKKKEVMP---IQSLDALYKER---KLOGKPGG 36
 Db 97 KCLGSGMKKEMIMSDAAYQRRALLIKRKREITEAPPG 137

RESULT 14
 ID FES_FSVST STANDARD; PRT; 477 AA.
 AC P00543;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).
 GN V-FES.
 OS Feline sarcoma virus (strain Snyder-Theilen).
 CC Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses.
 RN NCBI_TaxID=11780;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83050963; PubMed=6183005;
 RA Hampe A., Laprevotte I., Galibert F., Fedele L.A., Sherr C.J.;
 RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
 evidence for a family of tyrosine-specific protein kinase genes.";
 RT Cell 30:775-785(1982).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES
 POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
 SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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 CC EMBL: J02088; AAA43046.2; -
 DR PIR: A00652; TVAVCS.
 DR HSSP: P11362; IFGK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2.1.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR ProDom: PD000093; SH2.1.
 DR SMART: SM00252; SH2.1.
 DR SMART: SM00219; TYRK.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00001; SH2.1.
 KW Polyprotein; Tyrosine-protein kinase; Oncogene; Transferase;
 ATP-binding; Phosphorylation; SH2 domain.
 FT DOMAIN 115 204 PROTEIN KINASE.
 FT DOMAIN 216 477 SH2.
 FT NP_BIND 222 230 ATP (BY SIMILARITY).


```

FT BINDING 245 245 ATP (BY SIMILARITY).
FT ACT_SITE 338 338 BY SIMILARITY.
FT MOD_RES 368 368 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 477 AA: 53756 MW: 887EDB4E7A3BE5 CRC64:

Query Match
Best local Similarity 37.2%; DB 1; Length 477;
Matches 16; Conservative 7; Mismatches 7; Indels 13; Gaps 3;

QY 10 KRQVM-PSIOSLD-ALVKEKKLOGK-----GGGPPP 39
Db 11 KKVLOBALQALQVLCQAKLQAKLEQLGPGPPP 53

RESULT 15
FES_FELCA STANDARD: PRT: 820 AA.
AC P14238:
DT 01-JAN-1990 (rel. 13, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
GN FES OR FPS.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RM SEQUENCE FROM N.A.
RX MEDLINE=87198954; PubMed=3553615;
RA Roebroek A.J.M., Schaeken J.A., Onnekink C., Bloemers H.P.J.,
RA van de Ven W.J.M.,
RT "Structure of the feline c-fes/fps proto-oncogene: genesis of a
RT retroviral oncogene."
RL J. Virol. 61:2009-2016(1987).
CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FES/FPS
CC SUBFAMILY.
CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 FCH DOMAIN.
CC -----
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CC -----
DR EMBL: M16705: AAA30808.1: -
DR EMBL: M16666: AAA30808.1: JOINED.
DR EMBL: M16667: AAA30808.1: JOINED.
DR EMBL: M16668: AAA30808.1: JOINED.
DR EMBL: M16669: AAA30808.1: JOINED.
DR EMBL: M16670: AAA30808.1: JOINED.
DR EMBL: M16671: AAA30808.1: JOINED.
DR EMBL: M16706: AAA30808.1: JOINED.
DR EMBL: M16672: AAA30808.1: JOINED.
DR EMBL: M16673: AAA30808.1: JOINED.
DR EMBL: M16674: AAA30808.1: JOINED.
DR EMBL: M16698: AAA30808.1: JOINED.
DR EMBL: M16700: AAA30808.1: JOINED.
DR EMBL: M16701: AAA30808.1: JOINED.
DR EMBL: M16702: AAA30808.1: JOINED.
DR EMBL: M16704: AAA30808.1: JOINED.
DR PIR: A27824: TYCTPF.
DR HSSP: P11362: IFCK.
DR InterPro: IPR001060: Cdc15_Fes_CIP4.
DR InterPro: IPR000719: Euk_pkinase.
DR InterPro: IPR000980: SH2.
DR InterPro: IPR01245: Tyr_pkinase.
DR Pfam: PF00017: SH2; 1.

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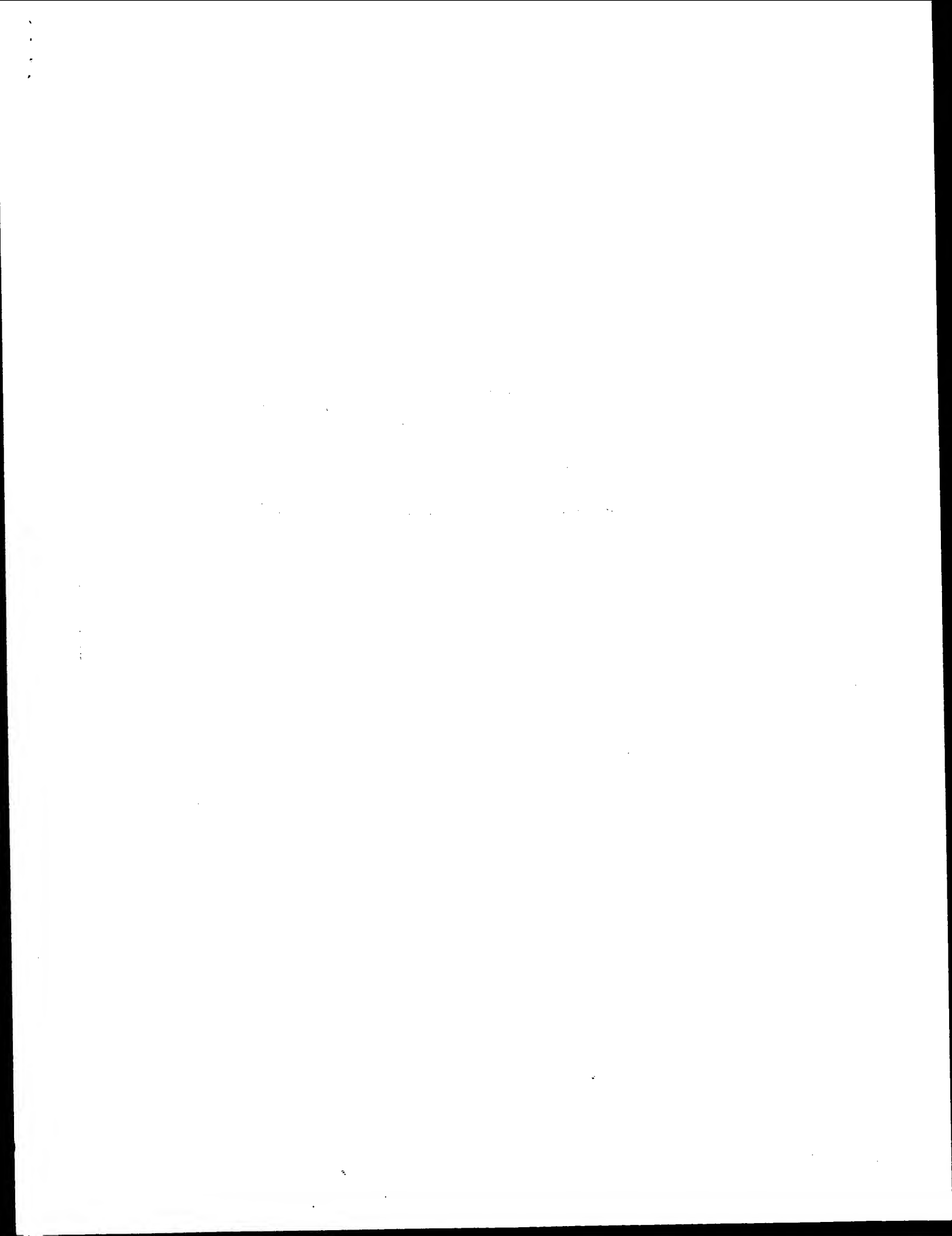
DR Pfam: PF00069: pkinase; 1.
DR InterPro: IPR00611: FCH; 1.
DR PRINTS: PRO0109: TYRKINASE.
DR ProDom: PD000001: Euk_pkinase; 1.
DR ProDom: PD000093: SH2; 1.
DR SMART: SM00055: FCH; 1.
DR SMART: SM00252: SH2; 1.
DR SMART: SM00219: TYRKC; 1.
DR PROSITE: PS50133: FCH; 1.
DR PROSITE: PS50107: PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011: PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50109: PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50001: SH2; 1.
KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain.
FT DOMAIN 1 94 FCH.
FT DOMAIN 458 547 SH2.
FT DOMAIN 559 820 PROTEIN_KINASE.
FT ND_BIND 565 573 ATP (BY SIMILARITY).
FT BINDING 588 588 ATP (BY SIMILARITY).
FT ACT_SITE 681 681 BY SIMILARITY.
FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 820 AA: 92974 MW: F3A52B750236834E CRC64:

Query Match
Best local Similarity 24.7%; DB 1; Length 820;
Matches 16; Conservative 7; Mismatches 7; Indels 13; Gaps 3;

QY 10 KRQVM-PSIOSLD-ALVKEKKLOGK-----GGGPPP 39
Db 354 KKVLOBALQALQVLCQAKLQAKLEQLGPGPPP 396

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Search completed: April 11, 2003, 16:11:57
Job time: 4.63322 secs



Mon Apr 14 14:01:23 2003

us-09-821-726a-13.rsp

Page 1

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 : Search time 10.8646 Seconds
(without alignments)
706.250 Million cell updates/sec

US-09-821-726a-13

Title: 994
Perfect score: 1 MKFTTFAGLGVFLPALA.....YTTSLVIMIVDISFCGDTVEN 185

Sequence: 1 MKFTTFAGLGVFLPALA.....YTTSLVIMIVDISFCGDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	984	99.0	199	1 C1IP_HUMAN	G9ns71 homo sapien
2	629	63.3	184	1 C1IP_MOUSE	G9cr16 mus musculu
3	95.5	9.6	719	1 NRPI_YEAST	P32770 saccharomyc
4	91	9.2	623	1 PNT1_DROME	P51022 drosophila
5	84.5	8.5	189	1 YHCN_BACSU	P54596 bacillus su
6	82.5	8.3	858	1 CYAG_DICDI	004101 dictyosteli
7	82	8.2	220	1 NUOB_ECOLI	P33598 escherichia
8	81	8.1	666	1 YEAT_YEAST	P40002 saccharomyc
9	81	8.1	828	1 MRKC_KLEPN	P21647 klebsiella
10	80	8.0	695	1 DVLI_MOUSE	P51141 mus musculu
11	80	8.0	749	1 MADI_YEAST	P40957 ratius norv
12	80	8.0	954	1 XNNA_MOUSE	P29126 schizosacch
13	80	8.0	954	1 XNNA_MOUSE	P33727 felis silve
14	80	8.0	954	1 XNNA_MOUSE	P33727 felis silve
15	79.5	7.9	535	1 ARSB_FELCA	P17442 saccharomyc
16	77.5	7.8	1341	1 PH81_YEAST	P05884 saccharomyc
17	77.5	7.8	1341	1 PH81_YEAST	P05884 saccharomyc
18	77.5	7.8	1341	1 PH81_YEAST	P05884 saccharomyc
19	77	7.7	1675	1 POL_RTBYP	P27502 rice tungro
20	75.5	7.6	191	1 CLRC_MOUSE	G910m0 mus musculu
21	75.5	7.6	296	1 PSFC_CLOPA	P55152 macaca mula
22	75.5	7.6	296	1 PSFC_CLOPA	P55152 macaca mula
23	75.5	7.6	296	1 PSFC_CLOPA	P55152 macaca mula
24	75.5	7.6	296	1 PSFC_CLOPA	P55152 macaca mula
25	75	7.5	1584	1 KYK1_DICDI	G22657 dictyosteli
26	74.5	7.5	457	1 PTK2_YEAST	P18160 dictyosteli
27	74.5	7.5	457	1 PTK2_YEAST	P18160 dictyosteli
28	74.5	7.5	457	1 PTK2_YEAST	P18160 dictyosteli
29	74	7.4	1956	1 HSF2_PLAFA	P04956 plasmodium
30	74	7.4	1956	1 HSF2_PLAFA	P04956 plasmodium
31	73.5	7.4	533	1 ARSB_HUMAN	P15848 homo sapien
32	73.5	7.4	533	1 ARSB_HUMAN	P15848 homo sapien
33	73.5	7.4	533	1 ARSB_HUMAN	P15848 homo sapien

RESULT 1	ID	CLIP_HUMAN	STANDARD	PRT	199 AA	ALIGNMENTS
AC	G9NS71					P40467 saccharomyc
DT	15-JUN-2002 (Rel. 41, Created)					P14248 plasmodium
DT	15-JUN-2002 (Rel. 41, Last sequence update)					P77885 lactobacill
DT	15-JUN-2002 (Rel. 41, Last annotation update)					P25159 drosophila
DE	CALL protein.					P07098 anabaena sp
GN	CALL.					P32944 saccharomyc
OS	Homo sapiens (Human).					P43101 cichorium l
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					P53840 saccharomyc
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					P54674 dictyosteli
OX	NCBI_TaxID=9606;					P15921 rickettsia
RN	SEQUENCE FROM N.A.					075829 homo sapien
RP	1					
RC	TISSUE=Stomach;					
RX	MEDLINE=20296773; PubMed=10835488;					
RA	Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;					
RT	Isolation of two novel genes, down-regulated in gastric cancer."					
RL	Upn. J Cancer Res. 91:459-463(2000).					
CC	-i- TISSUE SPECIFICITY: Expressed in stomach. No expression is					
CC	detected in cancer tissue or gastric cancer cell lines.					
CC	-----					
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CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; AB039886; BAA92433.1; "					
DR	MIM; 606402; "					
SO	SEQUENCE 199 AA: 21999 MW: C09988B9A133807A CRC64;					

Query Match 99.0%; Score 984; DB 1; Length 199;
Best Local Similarity 98.9%; Pred. No. 5.8e-84;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKFTTFAGLGVFLPALA.....YTTSLVIMIVDISFCGDTVEN 185	DB	1	MKFTTFAGLGVFLPALA.....YTTSLVIMIVDISFCGDTVEN 185
QY	15	NSIMDYNGEFAATRLFOKKTCTYHKKKKKEVMPSTOSLDALVEKKILOGGPGGPPKGLM 120	DB	15	NSIMDYNGEFAATRLFOKKTCTYHKKKKKEVMPSTOSLDALVEKKILOGGPGGPPKGLM 120
QY	61	NSIMDYNGEFAATRLFOKKTCTYHKKKKKEVMPSTOSLDALVEKKILOGGPGGPPKGLM 134	DB	61	NSIMDYNGEFAATRLFOKKTCTYHKKKKKEVMPSTOSLDALVEKKILOGGPGGPPKGLM 134
QY	121	YSVNNKXKDDLSKRGKNIANNKRCGIPPTMAEEMOASLFFSTCTYTTSLVIMIVDISFCG 180	DB	121	YSVNNKXKDDLSKRGKNIANNKRCGIPPTMAEEMOASLFFSTCTYTTSLVIMIVDISFCG 180
QY	135	YSVNNKXKDDLSKRGKNIANNKRCGIPPTMAEEMOASLFFSTCTYTTSLVIMIVDISFCG 194	DB	135	YSVNNKXKDDLSKRGKNIANNKRCGIPPTMAEEMOASLFFSTCTYTTSLVIMIVDISFCG 194
QY	181	DRVEN 185	DB	181	DRVEN 185
QY	195	DRVEN 199	DB	195	DRVEN 199

RESULT 2

C11P_MOUSE

ID C11P_MOUSE STANDARD: PRT: 184 AA.

AC 09CR36; 09D7K7; 09CT25;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE CALL protein homolog.

GN CALL

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai J Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Saito T., Okazaki Y., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,

RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M. J., Bull C., Fletcher C., Fujita M., Gariboldi M. F.,

RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,

RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitaker C., Wilmink L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

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CC EMBL: AK008990; BAB26010.1; -

CC EMBL: AK008622; BAB25784.1; -

CC EMBL: AK008641; BAB25801.1; -

CC EMBL: AK008647; BAB25805.1; -

CC EMBL: AK008722; BAB25856.1; -

CC EMBL: AK008745; BAB25872.1; -

CC EMBL: AK008933; BAB25975.1; -

CC EMBL: AK008956; BAB25988.1; -

CC EMBL: AK009145; BAB26103.1; -

CC EMBL: AK019050; BAB31525.1; -

CC MGD: MGI:191353; 220002K21Rik.

CC CONFLICT 113 113

CC SEQUENCE 184 AA; 20134 MM; 288582P040FFA8B CRC64;

SO Query Match

Best Local Similarity 63.3%; Score 629; DB 1; Length 184;

Matches 116; Conservative 25; Mismatches 40; Indels 4; Gaps 3;

RESULT 3

NRPI_YEAST

ID NRPI_YEAST STANDARD: PRT: 719 AA.

AC P32770; 012228;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Asparagine-rich protein (ARP protein).

GN NRPI OR ARP OR YDL167C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OX Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;

[1]

SEQUENCE FROM N.A.

RA STRAIN=AH22;

RA MEDLINE=93247548; PubMed=8483449;

RA Weiner E. P., Rao E., Brendel M.,

RA "Molecular structure and genetic regulation of SFA, a gene

RA responsible for resistance to formaldehyde in Saccharomyces

RA cerevisiae, and characterization of its protein product."

RA Mol. Gen. Genet. 237:351-358(1993).

RT [2]

RP SEQUENCE FROM N.A.

RA STRAIN=S288c;

RA Pohl T. M.;

RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.

CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).

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CC EMBL: X68020; CAA48159.1; -

CC EMBL: Z67750; CAA91579.1; -

CC EMBL: Z74215; CAA98741.1; -

CC PIR: S31139; S31139.

CC SGG: S0002326; NRPI.

CC InterPro: IPR000504; RNA_rec_mot.

CC InterPro: IPR001876; Znf_RanBP.

CC Pfam: PF000641; znf_RanBP.

CC Pfam: PF000641; znf_RanBP.

CC SMART: SM00347; znf_RanBP.

CC SMART: SM00347; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

CC PROSITE: PS0102; znf_RanBP.

Query Match

Best Local Similarity 9.6%; Score 95.5; DB 1; Length 719;

Matches 40; Conservative 18; Mismatches 62; Indels 37; Gaps 5;

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blaise R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Aguiar Y.A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Boriva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Genter A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garay N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Pollard D.R., Pacleb J.M., Reese M.G.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard D.R., Pacleb J.M., Reese M.G.,
 RA Reineert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Strydom R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-T., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RL [3]
 RN SPOUNCE OF 551-708 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL
 RP STRAIN.
 RC STRAIN-Canton-S; TISSUE-Larva;
 RX MEDLINE=92249640; PubMed=1577186;
 RA Chen T., Bunting M., Karim F.D., Thummel C.S.;
 RT "Isolation and characterization of five *Drosophila* genes that encode
 RT an ets-related DNA binding domain.";
 RL Dev. Biol. 151:176-191(1992).
 CC -1- FUNCTION: REQUIRED FOR GLIAL-NEURONAL CELL INTERACTIONS AT THE
 CC VENTRAL MIDLINE WHICH ARE NECESSARY FOR THE PROPER ELABORATION OF
 CC COMMISSURES IN THE EMBRYONIC CNS.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potentially).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: P1 (AC P1022) AND P2 (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A COMPLEX DYNAMIC PATTERN IN
 CC EARLY EMBRYOS, INCLUDING THE MIDLINE AND MIDLINE GLIAL CELLS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER
 CC LEVELS DURING LARVAL DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X6167; CA448917.1;
 DR EMBL: AE003742; AAF56125.1;
 DR EMBL: M88472; AAC34200.1;
 DR HSSP: P14921; 2STT.
 DR FlyBase: FBgn0003118; pnt.
 DR InterPro: IPR000418; Ets.

DR InterPro: IPR002341; HSF ETS.
 DR InterPro: IPR003118; SAM_PNT.
 DR Pfam: PF00178; Ets; 1.
 DR Pfam: PF02198; SAM_PNT; 1.
 DR PRINTS: PR00454; ETSDOMAIN.
 DR SMART: SM00413; ETS; 1.
 DR SMART: SM00251; SAM_PNT; 1.
 DR PROSITE: PS00345; ETS_DOMAIN_1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN_2; 1.
 DR PROSITE: PS00347; ETS_DOMAIN_3; 1.
 DR DNA-binding; Nuclear protein; Developmental protein;
 KW Alternative splicing.
 FT DOMAIN 166 250
 FT DOMAIN 341 347
 FT DOMAIN 359 362
 FT DOMAIN 389 392
 FT DOMAIN 405 415
 FT DOMAIN 418 421
 FT DOMAIN 481 484
 FT DNA_BIND 610 690
 FT CONFLICT 133 135
 SQ SEQUENCE 718 AA; 77683 MW; FDCAFDF0F4BCD69C5 CRC64;
 Query Match 9.2%; Score 91; DB 1; Length 718;
 Best local Similarity 27.1%; Pred. No. 0.9;
 Matches 38; Conservative 21; Mismatches 37; Indels 44; Gaps 8;
 Oy 15 LAPALANYIDVDDNNNGSGOOSVYNNH-----NNAVNNNGGWSNNDYNGCF 70
 Db 365 LPPAVQOSN---NENNNSSSTNNSSNNNNNGSSNNSSNNNNNNNNNNI-----NFM 417
 Oy 71 AATRIFFOKTCIVHKKKEVMPSTIOSLDAVKEKRLGKGGPGGPKGLMYSVNPKYDD 130
 Db 418 AAAATFQ-----HDKKE--PGTON-----GNIGYGGG-----SNQNDPTD 453
 Oy 131 ISKFGKNIANNMCGIPTYMA 150
 Db 454 LSSY-----GLPAHLA 464
 RESULT 6
 YHNC_BACSU STANDARD; PRT; 189 AA.
 AC P54598;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical lipoprotein yhnc precursor.
 GN YHNC.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124185; PubMed=8969498;
 RA Noback M.A., Terpstra P., Holtsappell S., Venema G., Bron S.;
 RT "A 22 kb DNA sequence in the *cspB-glpPKD* region at 75 degrees on the
 RL Microbiology 142:3021-3026(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.U., Conerton I.F., Cummings N.D., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emminger P.T.,
 RA Ertan K.D., Ertongton J., Fabret C., Ferreri E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Gallen D.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,


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RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT In the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
CC -I FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. DOES COUPLE THE REDOX REACTION TO PROTON
CC TRANSLLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
CC GRADIENT.
CC -I CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -I COPACOPAR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
CC -I SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS.
CC -I SIMILARITY: BELONGS TO THE COMPLEX I 20 kDa SUBUNIT FAMILY.
CC -I CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 89.
-----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb.sib.ch).
-----
CC DR EMBL, X68301; CAA48361.1; -.
CC DR EMBL, AE000318; AAC75347.1; -.
CC DR EMBL, D90860; BAA16122.1; ALT.FRAME.
CC DR EMBL, D90860; BAA16121.1; ALT.FRAME.
CC DR EMBL, AE005461; AAG57416.1; -.
CC DR EMBL, AP002561; BAB56594.1; -.
CC DR PIR, S37059; S37059.
CC DR PIR, S38311; S38311.
CC DR SWISS-2DPAGE, P33598; COLI.
CC DR Ecocore: EG12083; nuob.
CC DR InterPro: IPR002096; Cmp1x1_20kda.
CC DR Pfam, PF01058; oxidored_96; 1.
CC DR PROSITE, PS01150; COMPLEX_I_20K; 1.
CC KW Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S;
CC Complete proteome.
CC FT METAL 63 63 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 64 64 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 129 129 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 158 158 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT CONFLICT 71 71 S -> L (IN REF. 1).
CC SQ SEQUENCE 220 AA; 25056 MW; BBD62685059380 CRC64;
Query Match 8.2%; Score 82; DB 1; Length 220;
Best Local Similarity 18.4%; Pred. No. 1.5;
Matches 33; Conservative 25; Mismatches 47; Indels 74; Gaps 7;
QY 24 IDVDDNNNAGSGGQSV-----SYNNEHVAVYDNNNGNDNSIMDGNGFAATRLF 76
   |||::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Db 8 IDPMGENEDRYLOKEITVDPLEEQEVKNVYMGKLMDVNVNMGKRNIMPYNFGISC--- 63
QY 77 QKTKCIYHKMKKKEMVPSIQSIDALVKREKKLOGKGPGGPPEGLMYSVNPNKVDDLSEFGK 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 -----CYV-----EWVTSTFA-----VHDVARFG- 82
QY 137 NIAMNCGRIPTYMAEENGEASLEFFYSGTCYTVS-----LTWIDISFCDDT 182
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 --AEVLRASP-----ROADLMVAVGAGCFPKMAPVIQRLYLDQMLEPKWIVSMGCANCS 132
RESULT 9
YEAST_YEAST STANDARD; PRT; 666 AA.
AC PA0002:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 72.5 kDa protein in GCN4-WBp1 intergenic region.
VELOC7M.
```


[illegible]

CC - TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE BRAIN, TESTIS AND
 CC KIDNEY, LOWER LEVELS IN THE OVARY, BREAST, MUSCLE, LIVER AND SMALL
 CC INTESTINE, AND VERY LOW LEVELS ARE SEEN IN THE SPLEEN AND THYMUS.
 CC A MODERATE LEVEL EXPRESSION IS SEEN IN THE HEART.
 CC - DEVELOPMENTAL STAGE: IS EXPRESSED THROUGHOUT THE EMBRYONIC CENTRAL
 CC NERVOUS SYSTEM FROM PRESOMITE STAGES AND IN NEURON-RICH AREAS OF
 CC THE BRAIN THROUGHOUT POSTNATAL DEVELOPMENT, AS WELL AS IN MANY
 CC OTHER TISSUES.
 CC - SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 CC - SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -----
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 CC -----
 CC EMBL: U01015; AAA82175.1; -
 CC EMBL: U28138; AAA74049.1; -
 CC HSP: Q12923; 3PDZ.
 CC MGD: MGI:94941; DVI.
 CC InterPro: IPR000591; DEP.
 CC InterPro: IPR001158; DIX.
 CC InterPro: IPR003351; Dishevelled.
 CC InterPro: IPR001478; PDZ.
 CC Pfam: PF00595; PDZ; 1.
 CC Pfam: PF00610; DEP; 1.
 CC Pfam: PF00778; DIX; 1.
 CC Pfam: PF02377; Dishevelled; 1.
 CC ProDom: PD003639; DIX; 1.
 CC SMART: SM00021; DAX; 1.
 CC SMART: SM00049; DEP; 1.
 CC SMART: SM00228; PDZ; 1.
 CC PROSITE: PS50186; DEP; 1.
 CC PROSITE: PS50106; PDZ; 1.
 CC KMW Developmental protein.
 CC FT DOMAIN 251 323
 CC FT 425 499 PDZ.
 CC FT 390 393 DEP.
 CC FT 122 125 POLY-SER.
 CC FT CONFLICT 211 MISSING (IN REF. 2).
 CC FT CONFLICT 211 T->N (IN REF. 2).
 CC SO SEQUENCE 695 AA; 75350 MW; A9FA449F5C7F5F2 CRC64;
 CC -----
 CC Query Match 8.0%; Score 80; DB 1; Length 695;
 CC Best Local Similarity 25.7%; Pred. No. 9;
 CC Matches 28; Conservative 14; Mismatches 49; Indels 18; Gaps 5;
 CC -----
 CC QY 34 GSGQSVSVNNEHNVAVDNNMDSWNSIMDYGNCFATRLFOKKTCTVHKMKKEVMP 93
 CC DB 598 GSGSES-----DHTVPSGSGSTG-----WER-----PVSQLSRSGSS--PRSQAASAVAG 640
 CC QY 94 IQSLDALVKEKKLQGGKPGPPKGLMTSVNPKVLDLSKFGKNINMC 142
 CC DB 641 LPLPLHLTKAYAVVGGPPGPPVRELA-AVPELTGSRQSFQKAMGNPC 688
 CC -----
 CC RESULT 12
 CC DVL1_RAT
 CC ID DVL1_RAT STANDARD; PRT; 695 AA.
 CC AC Q9WVB9; Q9WVB8; Q9WUG5;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1)
 CC DE (DSH homolog 1).
 CC GN DVL1.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;

CC [1]
 CC SEQUENCE FROM N.A.
 CC RP STRAIN=Histar Kyoto;
 CC RX MEDLINE=21254118; PubMed=11354832;
 CC RA de Lange R.P.J., Burr K., Clark J.S., Negrin C.D., Brosnan M.J.,
 CC RA St Clair D.M., Komlenczak A.F., Shaw D.J.;
 CC RT "Mapping and sequencing rat dishevelled-1: a candidate gene for
 CC RT cerebral ischaemic insult in a rat model of stroke";
 CC RL Neurogenetics 3:99-106(2001)
 CC - FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC - SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC - SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC - SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF143545; AAD33896.2; -
 CC EMBL: AF143546; AAD33897.2; -
 CC EMBL: AF143548; AAD41492.2; -
 CC EMBL: AF143547; AAD41492.2; JOINED.
 CC EMBL: AF143550; AAD41493.1; -
 CC EMBL: AF143549; AAD41493.1; JOINED.
 CC InterPro: IPR000591; DEP.
 CC InterPro: IPR001158; DIX.
 CC InterPro: IPR003351; Dishevelled.
 CC InterPro: IPR001478; PDZ.
 CC Pfam: PF00595; PDZ; 1.
 CC Pfam: PF00610; DEP; 1.
 CC Pfam: PF00778; DIX; 1.
 CC Pfam: PF02377; Dishevelled; 1.
 CC ProDom: PD003639; DIX; 1.
 CC SMART: SM00021; DAX; 1.
 CC SMART: SM00049; DEP; 1.
 CC PROSITE: PS50186; DEP; 1.
 CC PROSITE: PS50106; PDZ; PARTIAL.
 CC KMW Developmental protein.
 CC FT DOMAIN 251 323
 CC FT 425 499 PDZ.
 CC FT 390 393 DEP.
 CC SO SEQUENCE 695 AA; 75447 MW; EEC4AA99A117D22A CRC64;
 CC -----
 CC Query Match 8.0%; Score 80; DB 1; Length 695;
 CC Best Local Similarity 25.7%; Pred. No. 9;
 CC Matches 28; Conservative 14; Mismatches 49; Indels 18; Gaps 5;
 CC -----
 CC QY 34 GSGQSVSVNNEHNVAVDNNMDSWNSIMDYGNCFATRLFOKKTCTVHKMKKEVMP 93
 CC DB 598 GSGSES-----DHTVPSGSGSTG-----WER-----PVSQLSRSGSS--PRSQAASAVAG 640
 CC QY 94 IQSLDALVKEKKLQGGKPGPPKGLMTSVNPKVLDLSKFGKNINMC 142
 CC DB 641 LPLPLHLTKAYAVVGGPPGPPVRELA-AVPELTGSRQSFQKAMGNPC 688
 CC -----
 CC RESULT 13
 CC MAD1_YEAST
 CC ID MAD1_YEAST STANDARD; PRT; 749 AA.
 CC AC P40957;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Spindle assembly checkpoint component MAD1 (Mitotic MAD1 protein).
 CC GN MAD1 OR YG1086M.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;

Mon Apr 14 14:01:18 2003

us-09-821-726a-13.rapb

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:11:18 : Search time 18.4095 Seconds
(without alignments)
614.367 Million cell updates/sec

Title: US-09-821-726a-13
Perfect score: 994
Sequence: 1 MKFTVAGLLGVFIAPALA.....YTSVLMIYDISFCDDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues
Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications-AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	984	99.0	185	US-09-992-598-211	Sequence 211, App
2	984	99.0	185	US-09-989-293A-211	Sequence 211, App
3	984	99.0	185	US-09-989-735-211	Sequence 211, App
4	984	99.0	185	US-09-990-444-211	Sequence 211, App
5	984	99.0	185	US-10-001-054-14	Sequence 14, Appl
6	984	99.0	185	US-09-989-730-211	Sequence 211, App
7	984	99.0	185	US-09-990-436-211	Sequence 211, App
8	984	99.0	185	US-09-991-181-211	Sequence 211, App
9	984	99.0	185	US-09-989-734-211	Sequence 211, App
10	984	99.0	185	US-09-993-653-211	Sequence 211, App
11	984	99.0	185	US-09-993-667-211	Sequence 211, App
12	984	99.0	185	US-09-990-562-211	Sequence 211, App
13	984	99.0	185	US-09-990-562-211	Sequence 211, App
14	984	99.0	185	US-09-997-428-211	Sequence 211, App
15	984	99.0	185	US-09-997-666-211	Sequence 211, App
16	984	99.0	185	US-10-227-884-148	Sequence 148, App
17	984	99.0	185	US-09-990-711-211	Sequence 211, App
18	984	99.0	185	US-10-230-163-148	Sequence 148, App
19	984	99.0	185	US-10-230-163-148	Sequence 148, App

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21	984	99.0	185	US-09-746-783-146	Sequence 146, App
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25	984	99.0	185	US-10-230-338-148	Sequence 148, App
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28	984	99.0	185	US-09-997-514-211	Sequence 211, App
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31	984	99.0	185	US-10-230-414-148	Sequence 211, App
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ALIGNMENTS

RESULT 1
US-09-992-598-211
Sequence 211, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13


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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1,4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1, 4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 3
US-09-989-735-211
Sequence 211, Application US//09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJawin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61

1	CURRENT APPLICATION NUMBER: US/09/989,735
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5	PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-09

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Query Match          99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.4e-95;
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RESULT 4
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Sequence 211, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Shelton, David
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE REFERENCE: P3034R1PCT
; CURRENT APPLICATION NUMBER: US/10/001.054
; CURRENT FILING DATE: 2001-11-30
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Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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: APPLICANT: Pan, James
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: APPLICANT: Roy, Margaret Ann
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/091360
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;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR APPLICATION NUMBER: 60/091544
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;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1,4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTVFAGLGVFLAPALANYIDVNDNNAGSGOOSVSYNNEHVAVYDNNNGDWSW 60
DB 1 MKFTVFAGLGVFLAPALANYINVDNNAGSGOOSVSYNNEHVAVYDNNNGDWSW 60
QY 61 NSTWDYGNFPAATRLFOKKTCTVHKMKKEYMPSIOSDALVKEKKLGKGPGPPKGLM 120
DB 61 NSTWDYGNFPAATRLFOKKTCTVHKMKKEYMPSIOSDALVKEKKLGKGPGPPKGLM 120
QY 121 YSVNPKKVDLSEFGKNIANMCRGIPTYMAEMQEASLFFYSCTCYTTSVLMIVDISFCG 180
DB 121 YSVNPKKVDLSEFGKNIANMCRGIPTYMAEMQEASLFFYSCTCYTTSVLMIVDISFCG 180
QY 181 DYVEN 185
DB 181 DYVEN 185

RESULT 7
US-09-990-436-211
; Sequence 211, Application US/09990436
; General Information:
; US20020198148A1
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-09

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKETVFAGLLEVFAPALANYNIDVNDNNNGSGOOSVSVNNEHVAVVDNNNGWDSW 60
DB 1 MKETVFAGLLEVFAPALANYNIDVNDNNNGSGOOSVSVNNEHVAVVDNNNGWDSW 60
OY 61 NSIMDYNGFAATRLFOKKTCIVHKMKKEVMPISIOSIDALVKEKKLOGKGGPPPKGLM 120
DB 61 NSIMDYNGFAATRLFOKKTCIVHKMKKEVMPISIOSIDALVKEKKLOGKGGPPPKGLM 120
OY 121 YSVNPKYVDLSKFGKNINMRCGIPTYAAEKEQASLFFYSGTCYTSVLWIVDISFCG 180
DB 121 YSVNPKYVDLSKFGKNINMRCGIPTYAAEKEQASLFFYSGTCYTSVLWIVDISFCG 180
OY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 8
US-09-991-181-211

Sequence 211, Application US/09991181
Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C53
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089908
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 ; PRIOR APPLICATION NUMBER: 60/090444
 ; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090445
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 ; PRIOR APPLICATION NUMBER: 60/090472
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 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB %; Length 185;
 Best Local Similarity 98.9%; Pred. No. 1.4e-95;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTTTFAGLGLVFLAPLANYNIDVNDNNAGSGQSVSYNNEHNVANYDNNNGWSW 60
 DB 1 MKFTTTFAGLGLVFLAPLANYNINVDNDNNAGSGQSVSYNNEHNVANYDNNNGWSW 60
 QY 61 NSIDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKKELCKGGGPPKGLM 120
 DB 61 NSIDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKKELCKGGGPPKGLM 120
 QY 121 YSVNPNKVDLSKFGKNIANNCRCIPTVMADEMOEASLFFYSGTCYTTYSVLAIVDISFCG 180
 DB 121 YSVNPNKVDLSKFGKNIANNCRCIPTVMADEMOEASLFFYSGTCYTTYSVLAIVDISFCG 180
 QY 181 DTVEN 185
 DB 181 DTVEN 185

RESULT 9
 US-09-993-687-211
 ; Sequence 211, Application US/09993687
 ; Publication No. US20020198149A1
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Klavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC11
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/993,687
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/090254
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PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431

1 PRIOR FILING DATE: 1998-06-24
2 PRIOR APPLICATION NUMBER: 60/090435
3 PRIOR FILING DATE: 1998-06-24
4 PRIOR APPLICATION NUMBER: 60/090444
5 PRIOR FILING DATE: 1998-06-24
6 PRIOR APPLICATION NUMBER: 60/090445
7 PRIOR FILING DATE: 1998-06-24
8 PRIOR APPLICATION NUMBER: 60/090472
9 PRIOR FILING DATE: 1998-06-24
10 PRIOR APPLICATION NUMBER: 60/090535
11 PRIOR FILING DATE: 1998-06-24
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16 PRIOR APPLICATION NUMBER: 60/090557
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18 PRIOR APPLICATION NUMBER: 60/090676
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21 PRIOR FILING DATE: 1998-06-25
22 PRIOR APPLICATION NUMBER: 60/090690
23 PRIOR FILING DATE: 1998-06-25
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38 PRIOR APPLICATION NUMBER: 60/091544
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41 PRIOR FILING DATE: 1998-07-02
42 PRIOR APPLICATION NUMBER: 60/091626
43 PRIOR FILING DATE: 1998-07-02
44 PRIOR APPLICATION NUMBER: 60/091633
45 PRIOR FILING DATE: 1998-07-02
46 PRIOR APPLICATION NUMBER: 60/091978
47 PRIOR FILING DATE: 1998-07-07
48 PRIOR APPLICATION NUMBER: 60/091982
49 PRIOR FILING DATE: 1998-07-07
50 PRIOR APPLICATION NUMBER: 60/092182
51 PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1,4e-95;
Matches 185; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAALANYNIDVNDNNAGSGOOSVSVNNEHNVANVNDNNNGWDSW 60
DB 1 MKFTIVFAGLLGVFLAALANYNIDVNDNNAGSGOOSVSVNNEHNVANVNDNNNGWDSW 60
QY 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVPSIOSIDLALVKKKLOGKCGGPPKGLM 120
DB 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVPSIOSIDLALVKKKLOGKCGGPPKGLM 120
QY 121 YSVNPNKVVDSLKFGKNANNCRGIPYMAFEKMEASLFFTSCTTYSVLMIYDISFCG 180
DB 121 YSVNPNKVVDSLKFGKNANNCRGIPYMAFEKMEASLFFTSCTTYSVLMIYDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 10
US-09-989-734-211
Sequence 211, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C64
CURRENT APPLICATION NUMBER: US/09/989, 734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1,4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIFACLLGVFLAPALANYNDVNDNNNGSGOOSVSVNNEHVAWVNDNNNGDSW 60
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DB 1 MKETIFACLLGVFLAPALANYNDVNDNNNGSGOOSVSVNNEHVAWVNDNNNGDSW 60
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QY 61 NSIWDYGNFPAATRIEFOKKTCTIVHKMKKEVMPISQISDALVYKCKILOGKGPGRPPKGLM 120
|||||
DB 61 NSIWDYGNFPAATRIEFOKKTCTIVHKMKKEVMPISQISDALVYKCKILOGKGPGRPPKGLM 120
|||||
QY 121 YSVNPKKVDLSKFGKNIANMKRGITPYMAEEMOENSLFFYSTGCTYTSVLMTVDISFCG 180
|||||
DB 121 YSVNPKKVDLSKFGKNIANMKRGITPYMAEEMOENSLFFYSTGCTYTSVLMTVDISFCG 180
|||||

QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 11
US-09-997-653-211

; Sequence 211, Application US/09997653
; Publication No. US20030008297A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C38
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US/09/997,653
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.4e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIVAGLGVLPALANYNIDVNDNNAGSGQOSVSVNNEHNVANDNNNGWDSW 60
DB 1 MKETIVAGLGVLPALANYNINVDNDNNAGSGQOSVSVNNEHNVANDNNNGWDSW 60
QY 61 NSIMDVGNGFAATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLQKGGPPPKGLM 120
DB 61 NSIMDVGNGFAATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLQKGGPPPKGLM 120

QY 121 YSVNPNKVDLSEKGNIANMCRGIPYMAEMQEASLFFYSGTCYTTSVLMIYDISPCG 180
DB 121 YSVNPNKVDLSEKGNIANMCRGIPYMAEMQEASLFFYSGTCYTTSVLMIYDISPCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 12

;; Sequence 211, Application US/09993667
;; Publication No. US2003002187A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerltzen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kjaavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C4
;; CURRENT APPLICATION NUMBER: US/09/993,667
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021

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58	PRIOR FILING DATE: 1998-07-07	59
59	PRIOR APPLICATION NUMBER: 60/091988	60
60	PRIOR FILING DATE: 1998-07-07	61
61	PRIOR APPLICATION NUMBER: 60/092182	62
62	PRIOR FILING DATE: 1998-07-09	63

Query Match	99.0%	Score 984	DB 9	Length 185
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Matches 183; Conservative	1	Mismatches	1	Indels 0; Gaps 0.
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Qy 1 MKFTVEAGLIGVFLAPALANYINIDVNDNNAGSGGQOSVYNNEHHYNAVVDNNNGWDSW 600
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QY      1 MKPTVEAGLIGVFLPALANINIDVDNNDNNAGSGOOSTSVNNEINVAVANDNNCKDWSW 60
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Db 1 MKFTIVFAGILGVFLAPALANYNINVDNNAGSGOOSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGEFAATRELFOKKTICIVHKMKKEVWPSIOSIDLATVKEKKLOGCGPPKGLM 120
Db 61 NSIWDYNGEFAATRELFOKKTICIVHKMKKEVWPSIOSIDLATVKEKKLOGCGPPKGLM 120
QY 121 YSVNPKWVDLSFGKNIANMCRGIPYMAEMQESLFFYSGTCYTTSVLMIYDISFCG 180
Db 121 YSVNPKWVDLSFGKNIANMCRGIPYMAEMQESLFFYSGTCYTTSVLMIYDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185
RESULT 13
US-09-990-438-211
Sequence 211, Application US/09990438
Publication No. US20030027754A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C3
CURRENT APPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091992
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 984; DB 9; Length 185;

Best Local Similarity 98.9%; Pred. No. 1, 4e-95;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTVFAGLGVFLPALANIVYDNDNNNAAGSQOQSVYVNEHNVANVDNNNGWDSW 60
 Db 1 MKFTVFAGLGVFLPALANIVYDNDNNNAAGSQOQSVYVNEHNVANVDNNNGWDSW 60
 QY 61 NSIWDYNGCFATRLFOKKTCTVHKMKKEWMPISQSLDLVYKKKLOGGPGGPPPKGLM 120
 Db 61 NSIWDYNGCFATRLFOKKTCTVHKMKKEWMPISQSLDLVYKKKLOGGPGGPPPKGLM 120
 QY 121 YSVNPKVDDLSKFGKNINMCRGIPYVAAEEMQEAFLFFYSQCTYTSVLWIVDISFCG 180
 Db 121 YSVNPKVDDLSKFGKNINMCRGIPYVAAEEMQEAFLFFYSQCTYTSVLWIVDISFCG 180
 QY 181 DTIVEN 185
 Db 181 DTIVEN 185

RESULT 14
 US-09-990-562-211
 ; Sequence 211, Application US/09990562
 ; Publication No. US20030027985A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C18
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/087106

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PRIOR APPLICATION NUMBER:	60/091982

;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09
Query Match 99.0%; Score 984; DB 9; Length 185;
Best Local Similarity 98.9%; Pred. No. 1,4e-95;
Matches 185; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MKETIVAGLIGVFLALPALANYNDVNDNNAGSGOOSVSVNNEHNANYNDNNNGMSW 60
QY 61 NSIWDYNGGAATRLFFCKKTCIVHKKKEVWPSIQSLDALVKKKLOGKGGPPKGLM 120
DB 61 NSIWDYNGGAATRLFFCKKTCIVHKKKEVWPSIQSLDALVKKKLOGKGGPPKGLM 120
QY 121 YSVNPNKVDLSKFGKNIAMNCRGIPYMAEEMQESLFFSGTCYTSVNIIVDISFCG 180
DB 121 YSVNPNKVDLSKFGKNIAMNCRGIPYMAEEMQESLFFSGTCYTSVNIIVDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185
RESULT 15
US-09-997-428-211
; Sequence 211, Application US/09997428
; Publication No. US20030027162A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301PC44
; CURRENT APPLICATION NUMBER: US/09/997,428
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
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;; PRIOR APPLICATION NUMBER: 60/087759
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;; PRIOR APPLICATION NUMBER: 60/087827
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;; PRIOR APPLICATION NUMBER: 60/088025
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;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
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;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/088212
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;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088555
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 : Search time 51.9086 Seconds
(without alignments)
474.899 Million cell updates/sec

Title: US-09-821-726a-13

Perfect score: 994
Sequence: 1 MKETIVFAGLGVFLAPALA.....YTSVLMIVDISFGDIYEN 185

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
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- 7: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
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- 20: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	984	99.0	185	20	AAW99667 Human secreted pro
2	984	99.0	185	21	AAW99667 Human PRO1005 prot
3	984	99.0	185	21	AAW99667 Human signal pept
4	984	99.0	185	21	AAW99667 Membrane-bound pro
5	984	99.0	185	22	AAW99667 Human PRO1005 (UNG
6	984	99.0	185	22	AAW99667 Human PRO1005 prot
7	984	99.0	185	23	AAW99667 Human angiogenesis
8	984	99.0	185	23	AAW99667 Human PRO1005 prot
9	984	99.0	185	23	AAW99667 Human PRO protein,
10	984	99.0	186	21	AAW99667 Human secreted pro

11	984	99.0	194	19	AAW99674 Cancer associated
12	984	99.0	194	20	AAW99674 Human ovarian tumo
13	602	60.6	184	23	AAW99674 Human ORF protein
14	189	19.0	184	21	AAW99674 Membrane-bound pro
15	189	19.0	184	22	AAW99674 Human PRO813 (UNG4
16	188	18.9	184	22	AAW99674 Human EST encoded
17	188	18.9	184	22	AAW99674 Human gene 14 enco
18	188	18.9	184	22	AAW99674 Human gene 14 enco
19	188	18.9	184	22	AAW99674 Human albumin fusi
20	188	18.9	184	23	AAW99674 Human PRO polypept
21	178	17.9	176	22	AAW99674 Human gene 14 enco
22	154.5	15.5	147	22	AAW99674 S cerevisiae apopt
23	95.5	9.6	719	22	AAW99674 Plasmodium falci
24	93	9.4	764	21	AAW99674 Plasmodium falci
25	93	9.4	1176	21	AAW99674 Plasmodium falci
26	91	9.2	718	22	AAW99674 Plasmodium falci
27	90	9.1	1245	21	AAW99674 Dictyostelium disc
28	88	8.9	286	22	AAW99674 Drosophila melano
29	84.5	8.5	2188	22	AAW99674 Plasmodium falci
30	84	8.5	1817	21	AAW99674 Plasmodium falci
31	83.5	8.4	1979	21	AAW99674 Sequence of the As
32	81.5	8.2	537	7	AAW99674 Oyster pearl prote
33	80.5	8.1	447	17	AAW99674 Plasmodium falci
34	80.5	8.1	652	18	AAW99674 Gene 21 human secr
35	80	8.0	280	21	AAW99674 Mouse Dishevelled-
36	80	8.0	695	22	AAW99674 Runinococcus flav
37	80	8.0	943	22	AAW99674 Drosophila melano
38	79.5	8.0	943	22	AAW99674 Plasmodium falci
39	78	7.8	540	21	AAW99674 Plasmodium falci
40	78	7.8	2539	21	AAW99674 Fungal ZBC protein
41	77.5	7.8	1341	23	AAW99674 Plasmodium falci
42	77.5	7.8	1714	21	AAW99674 A calcium-dependen
43	77	7.7	1316	21	AAW99674 Plasmodium falci
44	77	7.7	1337	21	AAW99674 Plasmodium falci
45	77	7.7	2010	21	AAW99674 Plasmodium falci

ALIGNMENTS

RESULT 1	
AAW99667	AAW99667 standard; Protein; 185 AA.
XX	XX
AC	AAW99667:
XX	XX
DT	07-JUN-1999 (first entry)
XX	XX
DE	Human secreted protein clone ej90_5 protein.
XX	XX
KW	Human; secreted protein; nutritional; cytokine; cell proliferation;
KW	tissue growth; chemotactic; chemokine; haematopoietic regulation;
KW	anti-inflammatory; cadherin; tumour invasion suppressor;
XX	XX
OS	tumour inhibition; gene therapy.
XX	XX
PN	Homo sapiens.
XX	XX
PD	W09907840-A1.
XX	XX
PF	18-FEB-1999.
XX	XX
XX	06-AUG-1998; 98MO-US16318.
PR	04-AUG-1998; 98US-0130189.
PR	06-AUG-1997; 97US-0906708.
XX	XX
PA	(GENY) GENETICS INST INC.
XX	XX
PI	Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
XX	Meiberg D, Racie LA, Steininger RJ, Treacy M;
DR	WPI: 1999-167419/14.

DR N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries

XX Claim 34; Page 98-99; 107pp; English.

CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccine) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.

XX Sequence 185 AA;

Query Match 99.0%; Score 984; DB 20; Length 185;

Best Local Similarity 98.9%; Pred. No. 3, 2e-93;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTVFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60

DB 1 MKFTVFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60

QY 61 NSIMWYGNFAATRLFOKKTCTVHKMKKEVMPISLQSLDLVYEKKILOGGPGGPPKGLM 120

DB 61 NSIMWYGNFAATRLFOKKTCTVHKMKKEVMPISLQSLDLVYEKKILOGGPGGPPKGLM 120

QY 121 YSVNPNKYVDLSKFKFNINAMCGIPTYVAEEMQASLFFYSCTCYTTSVLMIVDISFCG 180

DB 121 YSVNPNKYVDLSKFKFNINAMCGIPTYVAEEMQASLFFYSCTCYTTSVLMIVDISFCG 180

QY 181 DTVEN 185

DB 181 DTVEN 185

RESULT 2

AAB24067

ID AAB24067 standard; Protein; 185 AA.

AC AAB24067;

DT 29-JAN-2001 (first entry)

DE Human PRO1005 protein sequence SEQ ID NO:34.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotrophic; neuroprotective; anti-inflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophage disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.

OS Homo sapiens.

XX WO200053755-A2.

XX 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US00376.

XX 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;

XX WPI: 2000-572270/53.

XX N-PSDB; AAC58377.

PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -

XX Claim 61; Fig 22; 286pp; English.

CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO177, PRO809, PRO830, PRO848, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterized by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC glioma, astrocytoma, hypothalamic and other glandular, macrophage,
CC epithelial, stromal and blastocoele disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.

XX Sequence 185 AA;

Query Match 99.0%; Score 984; DB 21; Length 185;

Best Local Similarity 98.9%; Pred. No. 3, 2e-93;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTVFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60

DB 1 MKFTVFAGLLGVFLAPALANYINVDNDNNAGSGQGSVYNNENHNAVNDNNMGDSW 60

QY 61 NSIMWYGNFAATRLFOKKTCTVHKMKKEVMPISLQSLDLVYEKKILOGGPGGPPKGLM 120

DB 61 NSIMWYGNFAATRLFOKKTCTVHKMKKEVMPISLQSLDLVYEKKILOGGPGGPPKGLM 120

QY 121 YSVNPNKYVDLSKFKFNINAMCGIPTYVAEEMQASLFFYSCTCYTTSVLMIVDISFCG 180

DB 121 YSVNPNKYVDLSKFKFNINAMCGIPTYVAEEMQASLFFYSCTCYTTSVLMIVDISFCG 180

QY 181 DTVEN 185

DB 181 DTVEN 185

RESULT 3

AA87272

ID AA87272 standard; Protein; 185 AA.

XX AA87272;
AC AA87272;

DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSP-49 SFO ID NO:49.
XX
KW Human: signal peptide-containing protein; HSP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
PN W0200000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14484.
XX
PR 26-JUN-1998; 98US-0090762.
XX
PR 31-JUL-1998; 98US-0094983.
XX
PR 01-OCT-1998; 98US-0102686.
XX
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCYT-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI: 2000-160673/14.
DR N-PSDB: AAZ98157.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 193-194; 327pp; English.
XX
CC AA298109 to AA298242 encode AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
XX
Sequence 185 AA:
Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 3,2e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIVFAGLLGFLAPALANYNDVNDNNAGSGQGSVSYNNEHNAVNDNNNGWDSW 60
DB 1 MKETIVFAGLLGFLAPALANYNDVNDNNAGSGQGSVSYNNEHNAVNDNNNGWDSW 60
QY 61 NSIWDYGNCFATRLFPKKTCTVHKMKKEVMPSTSLDALVEKKLOGGPGPPPKGLM 120
DB 61 NSIWDYGNCFATRLFPKKTCTVHKMKKEVMPSTSLDALVEKKLOGGPGPPPKGLM 120
QY 121 YSVNPNKYDDLSKPKKNLANMCRGIPTYMAEEMOEASLFFYSGTCTTYSVLWIVDISFCG 180
DB 121 YSVNPNKYDDLSKPKKNLANMCRGIPTYMAEEMOEASLFFYSGTCTTYSVLWIVDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185
RESULT 4
AAY66686
ID AAY66686 standard; protein: 185 AA.
XX
AC AAY66686;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1005.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN W09963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0088990.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.

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PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 18-JUN-1998; 98US-0089601.
PR 18-JUN-1998; 98US-0089607.
PR 18-JUN-1998; 98US-0089608.
PR 19-JUN-1998; 98US-0089647.
PR 19-JUN-1998; 98US-0089648.
PR 19-JUN-1998; 98US-0089649.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090353.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 09-JUL-1998; 98US-0091982.
PR 10-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.

PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096947.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 98US-0115565.

XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WL, Yuan J;
XX
XX WPL: 2000-072883/06.
DR N-PSDB; AAZ65023.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 185 AA;
SQ
Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 3.2e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLGVFLAPLANYNIDVNDNNAGSGOOSVSVNNEHNVANVNNNGWDSM 60
Db 1 MKFTIVFAGLGVFLAPLANYNINVNDNNAGSGOOSVSVNNEHNVANVNNNGWDSM 60
QY 61 NSIWDYNGGFATRLPQKTCIVHKMKREVMPSIQSLDALYKEKKIQGPGGPPPKGLM 120
Db 61 NSIWDYNGGFATRLPQKTCIVHKMKREVMPSIQSLDALYKEKKIQGPGGPPPKGLM 120
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEMQASLFFYSGTCTYTTSLMIVDISFCG 180
Db 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEMQASLFFYSGTCTYTTSLMIVDISFCG 180
QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEMQASLFFYSGTCTYTTSLMIVDISFCG 180
Db 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEMQASLFFYSGTCTYTTSLMIVDISFCG 180

```


OY 181 DTVEN 185
 DB 181 DTVEN 185

RESULT 5
 AAB65209
 ID AAB65209 standard; Protein; 185 AA.
 AC AAB65209;
 XX 02-APR-2001 (first entry)

Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.

Human: secreted and transmembrane protein; PRO: cytosolic;
 cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 diagnostic assay.

Homo sapiens.

MO200073454-A1.

07-DEC-2000.

30-MAR-2000; 2000WO-US08439.

02-JUN-1999; 99WO-US12252.
 23-JUN-1999; 99US-0141037.
 07-JUL-1999; 99US-0143046.
 20-JUL-1999; 99US-0144758.
 26-JUL-1999; 99US-0145698.
 28-JUL-1999; 99US-0146222.
 17-AUG-1999; 99US-0149396.
 15-SEP-1999; 99WO-US21090.
 15-SEP-1999; 99WO-US21547.
 08-OCT-1999; 99US-0158663.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28301.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30911.
 05-JAN-2000; 2000WO-US00219.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 22-FEB-2000; 2000WO-US04414.
 24-FEB-2000; 2000WO-US04914.
 24-FEB-2000; 2000WO-US05004.
 02-MAR-2000; 2000WO-US05841.
 15-MAR-2000; 2000WO-US06884.
 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
 PI Zhang Z;

XX WPI: 2001-032160/04.
 DR N-PSDB: AAF44169.

PRO polynucleotides used to produce polypeptides used to target
 bioactive molecules such as toxins, radiolabels or antibodies, to
 specific cells, to cause targeted cell death -

Claim 12: Fig 139; 935pp; English.

The present invention describes human secreted and transmembrane PRO
 proteins. The PRO proteins have cytosolic activity. The PRO proteins
 can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 185 AA:

Query Match 99.0%; Score 984; DB 22; Length 185;
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKETIFAGILGVELAPALANYNDVDDNNNAGSQQSVSVNNEHNVAVNDNNNGDSW 60
 DB 1 MKETIFAGILGVELAPALANYINVDNNNAGSQQSVSVNNEHNVAVNDNNNGDSW 60

OY 61 NSIWDYGNFGFAATRLFOQKTCIVHKKKKEVMPSTQSDALVKKKILQGGKGGPPPKGLM 120
 DB 61 NSIWDYGNFGFAATRLFOQKTCIVHKKKKEVMPSTQSDALVKKKILQGGKGGPPPKGLM 120

OY 121 YSVNPKKVDPLSKFGKINNMCRGIPTYMAEEMQASLFPYSGCTYTSVLWIVDISFCG 180
 DB 121 YSVNPKKVDPLSKFGKINNMCRGIPTYMAEEMQASLFPYSGCTYTSVLWIVDISFCG 180

OY 181 DTVEN 185
 DB 181 DTVEN 185

RESULT 6
 AAB50957
 ID AAB50957 standard; Protein; 185 AA.
 XX AAB50957;
 AC AAB50957;
 XX 21-MAR-2001 (first entry)

Human PRO1005 protein.

Human: PRO: cytosolic; neurotropic; neuroprotective; respiratory general;
 antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 PRO agonist; cancer; inflammatory disorder; immunological disorder.

Homo sapiens.

MO200073348-A2.

07-DEC-2000.

30-MAY-2000; 2000WO-US14941.

02-JUN-1999; 99WO-US12252.
 22-JUN-1999; 99US-0140650.
 23-JUN-1999; 99US-0141037.
 20-JUL-1999; 99US-0144758.
 01-SEP-1999; 99WO-US20111.
 08-SEP-1999; 99WO-US20594.
 29-OCT-1999; 99US-0162506.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28634.
 02-DEC-1999; 99WO-US28551.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30999.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.

CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX
 SQ Sequence 185 AA:

Query Match 99.0%; Score 984; DB 23; Length 185;
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKFTVFAGLLGVFLPALANYNDVNDNNAGSGQSVSNNEHNVAVNDNNNGDSW 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MKFTVFAGLLGVFLPALANYNDVNDNNAGSGQSVSNNEHNVAVNDNNNGDSW 60
 OY 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120
 OY 121 YSNPNKVDLDFKFKNIAMKCRGIPTYMAEMQEAASLFYSGTCYTTSVLWTVDISFCG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 YSNPNKVDLDFKFKNIAMKCRGIPTYMAEMQEAASLFYSGTCYTTSVLWTVDISFCG 180
 OY 181 DTIVEN 185
 |||||
 DB 181 DTIVEN 185

RESULT 8
 ABB84886
 ID ABB84886 standard; Protein; 185 AA.

XX ABB84886;

DT 16-MAY-2002 (first entry)

DE Human PRO1005 protein sequence SEQ ID NO:140.

XX Human; angiogenesis; cardiact; cytoskeletal; antiangiogenic; hypotensive;
 KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

XX WO200200690-A2.

XX 03-JAN-2002.

PF 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000US-220664P.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-222695P.
 PR 23-AUG-2000; 2000US-222695P.
 PR 24-AUG-2000; 2000US-222695P.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-230978P.
 PR 24-SEP-2000; 2000US-230978P.
 PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.

XX (GETH) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gertlsten ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI: 2002-090516/12.

XX N-PSDB; ABL8814L.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX Claim 11; Fig 140; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytoskeletal,
 CC antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.

XX Sequence 185 AA:

Query Match 99.0%; Score 984; DB 23; Length 185;
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKFTVFAGLLGVFLPALANYNDVNDNNAGSGQSVSNNEHNVAVNDNNNGDSW 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1 MKFTVFAGLLGVFLPALANYNDVNDNNAGSGQSVSNNEHNVAVNDNNNGDSW 60
 OY 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 NSIMDYGNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLOGGPGPPKGLM 120
 OY 121 YSNPNKVDLDFKFKNIAMKCRGIPTYMAEMQEAASLFYSGTCYTTSVLWTVDISFCG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 YSNPNKVDLDFKFKNIAMKCRGIPTYMAEMQEAASLFYSGTCYTTSVLWTVDISFCG 180
 OY 181 DTIVEN 185
 |||||
 DB 181 DTIVEN 185

RESULT 9
AAU83665
ID AAU83665 standard; protein; 185 AA.
XX
AC AAU83665;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, seq ID No 148.
XX
XX Human: secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PE 29-JUN-2001; 2001MO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
XX
PR 25-JUL-2000; 2000US-220385P.
XX
PR 25-JUL-2000; 2000US-220605P.
XX
PR 25-JUL-2000; 2000US-220607P.
XX
PR 25-JUL-2000; 2000US-220624P.
XX
PR 25-JUL-2000; 2000US-220638P.
XX
PR 25-JUL-2000; 2000US-220664P.
XX
PR 25-JUL-2000; 2000US-220666P.
XX
PR 26-JUL-2000; 2000US-220893P.
XX
PR 28-JUL-2000; 2000MO-US20710.
XX
PR 23-AUG-2000; 2000MO-US23322.
XX
PR 24-AUG-2000; 2000MO-US23328.
XX
PR 15-SEP-2000; 2000US-000000P.
XX
PR 10-NOV-2000; 2000MO-US30873.
XX
PR 28-NOV-2000; 2000US-235646P.
XX
PR 01-DEC-2000; 2000MO-US32678.
XX
PR 20-DEC-2000; 2000US-0747259.
XX
PR 20-DEC-2000; 2000MO-US34956.
XX
PR 28-FEB-2001; 2001MO-US06520.
XX
PR 10-MAY-2001; 2001US-0854280.
XX
PR 25-MAY-2001; 2001MO-US17092.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Matanabe CK, Wood WI;
XX
DR WPI: 2002-172001/22.
XX
DR N-PSDB; ABK33609.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
PS Claim 11; Figure 148; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation of, or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 185 AA;
XX
Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 3.2e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MKFTTIFAGILGVFLAPALANYINDVDDNNAGSGQSVSVNNEHVAVYDNNNGDSW 60
DB 1 MKFTTIFAGILGVFLAPALANYINVDNNAGSGQSVSVNNEHVAVYDNNNGDSW 60
QY 61 NSIMWYGNFPAATRLFOKKTCTIVHKMKKEVMPSTQSIDALYKKEKLOGKGGPPPGGLM 120
DB 61 NSIMWYGNFPAATRLFOKKTCTIVHKMKKEVMPSTQSIDALYKKEKLOGKGGPPPGGLM 120
QY 121 YSVNPKKVDLSKFGKNIANMCRGIPYMAEMQEASLFFYSGTCYTSVLIVDISFCG 180
DB 121 YSVNPKKVDLSKFGKNIANMCRGIPYMAEMQEASLFFYSGTCYTSVLIVDISFCG 180
QY 181 DIVEN 185
DB 181 DIVEN 185
XX
RESULT 10
AAB38329
ID AAB38329 standard; protein; 186 AA.
XX
AC AAB38329;
XX
DT 31-JAN-2001 (first entry)
XX
DE Human secreted protein encoded by gene 9 clone HNSAD53.
XX
DE Immunosuppressive; antiarthritic; antitumour; antiproliferative;
KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;
XX
XX vulnerable; gene therapy; infection; secreted protein.
XX
OS Homo sapiens.
XX
XX WO200061623-A1.
XX
PD 19-OCT-2000.
XX
XX 06-APR-2000; 2000MO-US08979.
XX
XX 09-APR-1999; 99US-0128693.
XX
XX 26-APR-1999; 99US-0130991.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
XX Lafleur DW, Olsen HS, Edner R, Florence KA, Moore PA, Birse CE;
XX Young PE;
XX
DR WPI: 2000-647418/62.
XX
XX New nucleic acid molecules encoding 62 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives -
XX
PS Claim 11; Page 598; 716pp; English.
XX
XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
XX human secreted proteins encoded by the genes AAC69512-C69587. The genes
XX and proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated from

CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (any)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.

XX Sequence 186 AA;

Query Match 99.0%; Score 984; DB 21; Length 186;
 Best Local Similarity 98.9%; Pred. No. 3.2e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGLVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVAANDNNNGWDSW 60
 DB 1 MKFTIVFAGLGLVFLAPALANYNINVDNDNNAGSGQSVSVNNEHNVAANDNNNGWDSW 60
 QY 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVEKKLOGKGGCGPPPKGLM 120
 DB 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVEKKLOGKGGCGPPPKGLM 120
 QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQEASLFFYSGCTTYSVIMVIDISFCG 180
 DB 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQEASLFFYSGCTTYSVIMVIDISFCG 180
 QY 181 DTVEN 185
 DB 181 DTVEN 185

RESULT 11
 AAM69974

ID AAM69974 standard; Protein; 194 AA.

XX AAM69974;

DT 16-NOV-1998 (first entry)

XX Cancer associated protein.

KW Cancer; PCR: Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.

XX Synthetic.

OS WO9837187-A1.

PN 27-AUG-1998.

PD 18-FEB-1998; 98WO-JP00667.

PF 21-FEB-1997; 97JP-0052508.

PR (TAKI) TAKARA SHUZO CO LTD.

PA Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;

PI WPI: 1998-467552/40.

DR Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences

PS Claim 14; Page 64-65; 92pp; Japanese.

XX The cancer associated proteins AAM69974-W69976 where used in the method

CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.

XX Sequence 194 AA;

Query Match 99.0%; Score 984; DB 19; Length 194;
 Best Local Similarity 98.9%; Pred. No. 3.4e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLGLVFLAPALANYNIDVNDNNAGSGQSVSVNNEHNVAANDNNNGWDSW 60
 DB 10 MKFTIVFAGLGLVFLAPALANYNINVDNDNNAGSGQSVSVNNEHNVAANDNNNGWDSW 69
 QY 61 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVEKKLOGKGGCGPPPKGLM 120
 DB 70 NSIMDYNGGFAATRLFOKKTCTIVHKMKKEVMPSTIOSLDALVEKKLOGKGGCGPPPKGLM 129
 QY 121 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQEASLFFYSGCTTYSVIMVIDISFCG 180
 DB 130 YSVNPNKVDLSKFGKNIANNCRGIPITYMAEEMQEASLFFYSGCTTYSVIMVIDISFCG 189
 QY 181 DTVEN 185
 DB 190 DTVEN 194

RESULT 12
 AAY76591

ID AAY76591 standard; Protein; 194 AA.

XX AAY76591;

DT 10-APR-2000 (first entry)

XX Human ovarian tumor EST fragment encoded protein 87.

KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.

XX Homo sapiens.

OS DE19817557-A1.

PN 21-OCT-1999.

PD 09-APR-1998; 98DE-1017557.

PF 09-APR-1998; 98DE-1017557.

PR (METRA-) METAGEN GES GENOMFORSCHUNG MBH.

PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

PI WPI: 1999-591920/51.

DR N-PSDB; AA277487.
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents

PS Claim 25; Page 279; 310pp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which

CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of the
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor CDNA library derived EST
 CC fragments represented in AAZ77450-277572.

XX Sequence 194 AA;

Query Match 99.0%; Score 984; DB 20; Length 194;
 Best Local Similarity 98.9%; Pred. No. 3.4e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLPALANYNIDVNDNNAGSGQGSVSYNNEHNVANVDNNNGWDSW 60
 Db 10 MKFTIVFAGLLGVFLPALANYNINVDNNAGSGQGSVSYNNEHNVANVDNNNGWDSW 69

QY 61 NSIWDYNGGFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPPKGLM 120
 Db 70 NSIWDYNGGFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPPKGLM 129

QY 121 YSVNPNKVDLSKFGKNANMCRGIPTYMAEMQESLFFYSGTCYTSVLTWIDISFCG 180
 Db 130 YSVNPNKVDLSKFGKNANMCRGIPTYMAEMQESLFFYSGTCYTSVLTWIDISFCG 189

QY 181 DTVEN 185
 Db 190 DTVEN 194

RESULT 13
 ABP09922
 ID ABP09922 standard; Protein; 184 AA.

XX
 AC ABP09922;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human ORFX protein sequence SEQ ID NO:19826.

XX
 KW Human: open reading frame; ORFX: gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

XX
 OS Homo sapiens.
 XX
 PN WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US10836.
 XX
 PR 30-MAY-2000; 2000US-206132P.
 XX
 PR 29-AUG-2000; 2000US-228716P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach MD;

XX
 DR WPI: 2002-106308/14.
 DR N-PSDB: ABN25674.
 XX
 PR Novel human polypeptides and polynucleotides useful for diagnosing,
 PR preventing and treating cardiovascular disease, neurodegenerative,
 PR hyperproliferative disorders and autoimmune disorders
 PS Disclosure; SEQ ID 19826; 1037pp; English.

XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1
 CC in the specification), ABN15762 to ABN27232 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with an ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 184 AA;

Query Match 60.6%; Score 602; DB 23; Length 184;
 Best Local Similarity 60.5%; Pred. No. 7.3e-54;
 Matches 112; Conservative 28; Mismatches 41; Indels 4; Gaps 3;

QY 1 MKFTIVFAGLLGVFLPALANYNIDVNDNNAGSGQGSVSYNNEHNVANVDNNNGWDS 59
 Db 1 MKFTIVFAGLLGVFLPALANYNIDVNDNNAGSGQGSVSYNNEHNVANVDNNNGWDS 59

QY 60 WNSIWDYNGGFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPPKGL 119
 Db 60 WNSIWDYNGGFATRLFOKKTCTIVHKMKKEVMPSTOSLDALVKEKKLOGKGGPPPKGL 117

QY 120 YSVNPNKVDLSKFGKNANMCRGIPTYMAEMQESLFFYSGTCYTSVLTWIDISFCG 179
 Db 118 YSVNPNKVDLSKFGKNANMCRGIPTYMAEMQESLFFYSGTCYTSVLTWIDISFCG 177

QY 180 GDYVE 184
 Db 178 ETSVE 182

RESULT 14
 AAY66690
 ID AAY66690 standard; Protein; 184 AA.

XX
 AC AAY66690;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO813.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping.
 XX
 OS Homo sapiens.

```

XX  MO9963088-A2.
XX
XX  09-DEC-1999.
XX
XX  02-JUN-1999; 99MO-US12252.
XX
PR  02-JUN-1998; 98US-0087607.
PR  02-JUN-1998; 98US-0087609.
PR  03-JUN-1998; 98US-0087759.
PR  04-JUN-1998; 98US-0087827.
PR  04-JUN-1998; 98US-0088021.
PR  04-JUN-1998; 98US-0088025.
PR  04-JUN-1998; 98US-0088028.
PR  04-JUN-1998; 98US-0088029.
PR  04-JUN-1998; 98US-0088030.
PR  04-JUN-1998; 98US-0088033.
PR  05-JUN-1998; 98US-0088326.
PR  05-JUN-1998; 98US-0088167.
PR  05-JUN-1998; 98US-0088202.
PR  05-JUN-1998; 98US-0088212.
PR  09-JUN-1998; 98US-0088217.
PR  10-JUN-1998; 98US-0088655.
PR  10-JUN-1998; 98US-0088730.
PR  10-JUN-1998; 98US-0088734.
PR  10-JUN-1998; 98US-0088738.
PR  10-JUN-1998; 98US-0088740.
PR  10-JUN-1998; 98US-0088741.
PR  10-JUN-1998; 98US-0088810.
PR  10-JUN-1998; 98US-0088811.
PR  10-JUN-1998; 98US-0088824.
PR  10-JUN-1998; 98US-0088825.
PR  11-JUN-1998; 98US-0088826.
PR  11-JUN-1998; 98US-0088858.
PR  11-JUN-1998; 98US-0088861.
PR  11-JUN-1998; 98US-0088863.
PR  11-JUN-1998; 98US-0088876.
PR  12-JUN-1998; 98US-0089090.
PR  12-JUN-1998; 98US-0089105.
PR  16-JUN-1998; 98US-0089440.
PR  16-JUN-1998; 98US-0089512.
PR  17-JUN-1998; 98US-0089532.
PR  17-JUN-1998; 98US-0089538.
PR  17-JUN-1998; 98US-0089598.
PR  17-JUN-1998; 98US-0089599.
PR  17-JUN-1998; 98US-0089600.
PR  18-JUN-1998; 98US-0089653.
PR  18-JUN-1998; 98US-0089801.
PR  18-JUN-1998; 98US-0089907.
PR  19-JUN-1998; 98US-0089908.
PR  19-JUN-1998; 98US-0089947.
PR  19-JUN-1998; 98US-0089948.
PR  22-JUN-1998; 98US-0089952.
PR  22-JUN-1998; 98US-0090246.
PR  22-JUN-1998; 98US-0090252.
PR  23-JUN-1998; 98US-0090254.
PR  23-JUN-1998; 98US-0090349.
PR  24-JUN-1998; 98US-0090355.
PR  24-JUN-1998; 98US-0090429.
PR  24-JUN-1998; 98US-0090431.
PR  24-JUN-1998; 98US-0090435.
PR  24-JUN-1998; 98US-0090444.
PR  24-JUN-1998; 98US-0090445.
PR  24-JUN-1998; 98US-0090461.
PR  24-JUN-1998; 98US-0090472.
PR  24-JUN-1998; 98US-0090535.
PR  24-JUN-1998; 98US-0090538.
PR  24-JUN-1998; 98US-0090540.
PR  24-JUN-1998; 98US-0090557.
PR  25-JUN-1998; 98US-0090676.
XX
XX  25-JUN-1998; 98US-0090678.
PR  25-JUN-1998; 98US-0090688.
PR  25-JUN-1998; 98US-0090690.
PR  25-JUN-1998; 98US-0090691.
PR  25-JUN-1998; 98US-0090694.
PR  25-JUN-1998; 98US-0090695.
PR  25-JUN-1998; 98US-0090696.
PR  26-JUN-1998; 98US-0090862.
PR  26-JUN-1998; 98US-0090863.
PR  01-JUL-1998; 98US-0091358.
PR  01-JUL-1998; 98US-0091360.
PR  02-JUL-1998; 98US-0091544.
PR  02-JUL-1998; 98US-0091478.
PR  02-JUL-1998; 98US-0091486.
PR  02-JUL-1998; 98US-0091519.
PR  02-JUL-1998; 98US-0091626.
PR  02-JUL-1998; 98US-0091628.
PR  02-JUL-1998; 98US-0091633.
PR  02-JUL-1998; 98US-0091646.
PR  07-JUL-1998; 98US-0091673.
PR  07-JUL-1998; 98US-0091978.
PR  09-JUL-1998; 98US-0091982.
PR  10-JUL-1998; 98US-0092182.
PR  10-JUL-1998; 98US-0092472.
PR  30-JUL-1998; 98US-0093339.
PR  04-AUG-1998; 98US-0094651.
PR  04-AUG-1998; 98US-0095282.
PR  04-AUG-1998; 98US-0095285.
PR  04-AUG-1998; 98US-0095301.
PR  04-AUG-1998; 98US-0095302.
PR  04-AUG-1998; 98US-0095318.
PR  04-AUG-1998; 98US-0095321.
PR  04-AUG-1998; 98US-0095325.
PR  10-AUG-1998; 98US-0095916.
PR  10-AUG-1998; 98US-0095929.
PR  10-AUG-1998; 98US-0096143.
PR  11-AUG-1998; 98US-0096146.
PR  12-AUG-1998; 98US-0096329.
PR  17-AUG-1998; 98US-0096757.
PR  17-AUG-1998; 98US-0096766.
PR  17-AUG-1998; 98US-0096768.
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PR  17-AUG-1998; 98US-0096791.
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PR  17-AUG-1998; 98US-0096891.
PR  17-AUG-1998; 98US-0096894.
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PR  18-AUG-1998; 98US-0096949.
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PR  18-AUG-1998; 98US-0096959.
PR  18-AUG-1998; 98US-0096960.
PR  18-AUG-1998; 98US-0097022.
PR  19-AUG-1998; 98US-0097141.
PR  20-AUG-1998; 98US-0097218.
PR  24-AUG-1998; 98US-0097661.
PR  26-AUG-1998; 98US-0097951.
PR  26-AUG-1998; 98US-0097952.
PR  26-AUG-1998; 98US-0097954.
PR  26-AUG-1998; 98US-0097955.
PR  26-AUG-1998; 98US-0097971.
PR  26-AUG-1998; 98US-0097974.
PR  26-AUG-1998; 98US-0097978.
PR  26-AUG-1998; 98US-0097979.
PR  26-AUG-1998; 98US-0097986.
PR  31-AUG-1998; 98US-0098014.
PR  16-SEP-1998; 98US-0098525.
PR  12-JAN-1999; 99US-01100634.
XX
XX  (GFTH ) GENENTECH INC.
PA
XX

```

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX
 DR WPI: 2000-072883/06.
 DR N-PSDB; AAB65029.
 XX
 PT Membrane-bound proteins and related nucleotide sequences
 PS
 XX claim 12; Fig 149; 822pp; English.
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 CC
 SQ Sequence 184 AA;
 Query Match 19.0%; Score 189; DB 21; Length 184;
 Best Local Similarity 27.1%; Pred. No. 2.6e-11;
 Matches 52; Conservative 40; Mismatches 78; Indels 22; Gaps 4;
 QY 1 MKFTVFAGLLGVFLAPALANYINDVNDNNAAGSGQSVSNVNEHNVANVDNNGWDSW 60
 DB 1 MKILVAFVLVLTIFGIQSGYEVFNLISSNNGVQETITDNEKNTAIVNHAGSCSS 60
 QY 61 NSIMDYGNGFAATRLFEQKTCIVHKMKKEVMDISGLDAIVKEKILQGGCGPPPKGLM 120
 DB 61 TTTFDKHGYIASRVLSRACFLIKMDHONIPPLNLMOWIYEKQALDN-----M 110
 QY 121 VS-----VAPKNVVDLSK-----FGKNIANMCRGIPTYMAEMOEASLFFYSGTCYTT 169
 DB 111 FSNKYTWKYNPLESLIKQVDFLGSPIELCKHILPYLKG-EVENTHNVAGGCGAKAG 169
 QY 170 VLMIVDISFCGD 181
 DB 170 LIGIGISICAD 181
 RESULT 15
 AAB65213
 ID AAB65213 standard; Protein; 184 AA.
 XX
 AC AAB65213;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO813 (UNQ465) protein sequence SEQ ID NO:221.
 XX
 KW Human: secreted and transmembrane protein; PRO: cytosolic;
 KW cell death, cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146322.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03365.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 DR WPI: 2001-032160/04.
 DR N-PSDB: AAF41175.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 PS
 XX Claim 12; Fig 149; 935pp; English.
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 SQ Sequence 184 AA;
 Query Match 19.0%; Score 189; DB 22; Length 184;
 Best Local Similarity 27.1%; Pred. No. 2.6e-11;
 Matches 52; Conservative 40; Mismatches 78; Indels 22; Gaps 4;
 QY 1 MKFTVFAGLLGVFLAPALANYINDVNDNNAAGSGQSVSNVNEHNVANVDNNGWDSW 60
 DB 1 MKILVAFVLVLTIFGIQSGYEVFNLISSNNGVQETITDNEKNTAIVNHAGSCSS 60
 QY 61 NSIMDYGNGFAATRLFEQKTCIVHKMKKEVMDISGLDAIVKEKILQGGCGPPPKGLM 120
 DB 61 TTTFDKHGYIASRVLSRACFLIKMDHONIPPLNLMOWIYEKQALDN-----M 110
 QY 121 VS-----VAPKNVVDLSK-----FGKNIANMCRGIPTYMAEMOEASLFFYSGTCYTT 169
 DB 111 FSNKYTWKYNPLESLIKQVDFLGSPIELCKHILPYLKG-EVENTHNVAGGCGAKAG 169
 QY 170 VLMIVDISFCGD 181

Mon Apr 14 14:01:13 2003

us-09-821-726a-13.rag

Page 13

Db 170 LGLGISICAD 181

Search completed: April 11, 2003, 16:11:10
Job time : 53.9086 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:06:33 : Search time 3.92822 Seconds
(without alignments)
474.899 Million cell updates/sec

Title: US-09-821-726a-3
Perfect score: 81
Sequence: 1 KKLGGKGGCGPPK 14

Scoring table:
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Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	185	20	AAW99667
2	81	100.0	185	21	AAW99667
3	81	100.0	185	21	AAW99667
4	81	100.0	185	21	AAW99667
5	81	100.0	185	22	AAW99667
6	81	100.0	185	22	AAW99667
7	81	100.0	185	22	AAW99667
8	81	100.0	185	23	AAW99667
9	81	100.0	185	23	AAW99667
10	81	100.0	186	21	AAW99667

11	81	100.0	194	19	AAW99667
12	81	100.0	194	20	AAW99667
13	52	64.2	103	21	AAW99667
14	52	64.2	103	21	AAW99667
15	52	64.2	103	21	AAW99667
16	52	64.2	103	21	AAW99667
17	52	64.2	103	21	AAW99667
18	52	64.2	103	21	AAW99667
19	51	63.0	108	22	AAW99667
20	51	63.0	108	22	AAW99667
21	50.5	62.3	140	22	AAW99667
22	49.5	61.1	147	22	AAW99667
23	49	60.5	84	22	AAW99667
24	49	60.5	115	22	AAW99667
25	49	60.5	120	22	AAW99667
26	49	60.5	855	22	AAW99667
27	49	60.5	855	22	AAW99667
28	48	59.3	127	22	AAW99667
29	48	59.3	128	22	AAW99667
30	48	59.3	247	20	AAW99667
31	48	59.3	247	20	AAW99667
32	48	59.3	532	21	AAW99667
33	48	59.3	774	21	AAW99667
34	48	59.3	2061	22	AAW99667
35	47.5	58.6	109	22	AAW99667
36	47	58.0	71	22	AAW99667
37	47	58.0	102	22	AAW99667
38	47	58.0	1963	22	AAW99667
39	46.5	57.4	127	22	AAW99667
40	46	56.8	99	22	AAW99667
41	46	56.8	114	22	AAW99667
42	46	56.8	125	22	AAW99667
43	46	56.8	133	22	AAW99667
44	46	56.8	135	22	AAW99667
45	46	56.8	141	22	AAW99667

ALIGNMENTS

RESULT 1

AAW99667

ID AAW99667 standard: Protein; 185 AA.

XX

AC AAW99667;

XX

DT 07-JUN-1999 (first entry)

XX

DE Human secreted protein clone ej90_5 protein.

XX

KW Human: secreted protein; nutritional; cytokine; cell proliferation;

KW differentiation; immune stimulating; vaccine; haematopoiesis; regulation;

KW tissue growth; chemotactic; chemokine; haemostatic; thrombolytic;

KW anti-inflammatory; cadherin; tumour invasion suppressor;

KW tumour inhibition; gene therapy.

XX

OS Homo sapiens.

OS

PN WO9907840-A1.

PN

PD 18-FEB-1999.

PD

PF 06-AUG-1998; 98MO-US16318.

PF

PR 04-AUG-1998; 98US-0130189.

PR

PA 06-AUG-1997; 97US-0906708.

PA

XX (GENE) GENETICS INST INC.

XX

PI Agostino M, Evans C, Jacobs K, Lavallie ER, McCoy JM;

PI Werberg D, Kacie LA, Steindinger RJ, Treacy M;

XX

WP1: 1999-167419/14.

Cancer associated

Human ovarian tumor

Human ORF ORF812

Human ORF4050 prot

Human polypeptide

Human DNA modifica

Human protein sequ

Human polypeptide

Human polypeptide

Human polypeptide

Escherichia coli U

Human polypeptide

Human polypeptide

Human polypeptide

Human polypeptide

Human protease pol

Human metallopept

Human polypeptide

Human polypeptide

Polypeptide fragme

Human secreted pro

Human ORF ORF2306

Drosophila melanog

Drosophila melanog

Human polypeptide

Propionibacterium

Human polypeptide

Drosophila melanog

Human polypeptide

Human polypeptide

Human polypeptide

Human polypeptide

Human polypeptide

DR N-PSDB: AAX19493.
 XX
 PT New polynucleotides encoding secreted human proteins - derived from
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
 PT or adult retina cDNA libraries
 XX
 PS Claim 34; Page 98-99; 107pp; English.
 XX
 CC The present sequence represents a human secreted protein. The secreted
 CC protein can have activities such as: nutritional activity, cytokine and -
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. The
 CC polynucleotides are also stated to be useful for gene therapy.
 XX
 SQ Sequence 185 AA:
 Query Match 100.0%; Score 81; DB 20; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLQGGPGGPPPK 14
 DB 104 KKLQGGPGGPPPK 117
 RESULT 2
 AAB24067
 ID AAB24067 standard; Protein: 185 AA.
 XX
 AC AAB24067;
 XX
 DT 29-JAN-2001 (first entry)
 DE Human PRO1005 protein sequence SEQ ID NO:14.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glial disorder; astrocyt disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophage disorder;
 KW epithelial disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immunologic disorder.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200053755-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 06-JAN-2000; 2000WO-US00376.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WT;

DR WPI: 2000-572270/53.
 DR N-PSDB: AAC58377.
 XX
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 XX
 PS Claim 61; Fig 22; 286pp; English.
 XX
 CC The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds maybe used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoele disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 185 AA:
 Query Match 100.0%; Score 81; DB 21; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KKLQGGPGGPPPK 14
 DB 104 KKLQGGPGGPPPK 117
 RESULT 3
 AAY87272
 ID AAY87272 standard; Protein: 185 AA.
 XX
 AC AAY87272;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSP-49 SEQ ID NO:49.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR N-PSDB: AAZ98157.
DR
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 193-194; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases), schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring) in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
SQ Sequence 185 AA;
XX
Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KKIQKGPGGPPK 14
Db 104 KKIQKGPGGPPK 117
IIIIIIIIIIII
RESULT 4
ID AAY6686 standard; protein: 185 AA.
XX
XX AAY6686;
AC
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1005.
XX
XX Membrane-bound polypeptide: PRO polypeptide: LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
XX WO963088-A2.
XX
XX PD 09-DEC-1999.
XX

PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088255.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 19-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 22-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.

PR	25-JUN-1998;	98US-0096095;
PR	25-JUN-1998;	98US-0096096;
PR	26-JUN-1998;	98US-0098062;
PR	26-JUN-1998;	98US-0098063;
PR	01-JUL-1998;	98US-0091358;
PR	01-JUL-1998;	98US-0091360;
PR	01-JUL-1998;	98US-0091544;
PR	02-JUL-1998;	98US-0091478;
PR	02-JUL-1998;	98US-0091486;
PR	02-JUL-1998;	98US-0091519;
PR	02-JUL-1998;	98US-0091626;
PR	02-JUL-1998;	98US-0091628;
PR	02-JUL-1998;	98US-0091633;
PR	02-JUL-1998;	98US-0091646;
PR	02-JUL-1998;	98US-0091673;
PR	07-JUL-1998;	98US-0091978;
PR	07-JUL-1998;	98US-0091982;
PR	09-JUL-1998;	98US-0092182;
PR	10-JUL-1998;	98US-0092472;
PR	20-JUL-1998;	98US-0093339;
PR	30-JUL-1998;	98US-0094651;
PR	04-AUG-1998;	98US-0095285;
PR	04-AUG-1998;	98US-0095285;
PR	04-AUG-1998;	98US-0095301;
PR	04-AUG-1998;	98US-0095302;
PR	04-AUG-1998;	98US-0095318;
PR	04-AUG-1998;	98US-0095321;
PR	04-AUG-1998;	98US-0095325;
PR	10-AUG-1998;	98US-0095916;
PR	10-AUG-1998;	98US-0095929;
PR	10-AUG-1998;	98US-0096012;
PR	11-AUG-1998;	98US-0096143;
PR	11-AUG-1998;	98US-0096146;
PR	12-AUG-1998;	98US-0096329;
PR	17-AUG-1998;	98US-0096757;
PR	17-AUG-1998;	98US-0096766;
PR	17-AUG-1998;	98US-0096768;
PR	17-AUG-1998;	98US-0096773;
PR	17-AUG-1998;	98US-0096791;
PR	17-AUG-1998;	98US-0096867;
PR	17-AUG-1998;	98US-0096891;
PR	17-AUG-1998;	98US-0096894;
PR	17-AUG-1998;	98US-0096895;
PR	17-AUG-1998;	98US-0096897;
PR	18-AUG-1998;	98US-0096949;
PR	18-AUG-1998;	98US-0096950;
PR	18-AUG-1998;	98US-0096959;
PR	18-AUG-1998;	98US-0096960;
PR	18-AUG-1998;	98US-0097022;
PR	19-AUG-1998;	98US-0097141;
PR	20-AUG-1998;	98US-0097218;
PR	24-AUG-1998;	98US-0097661;
PR	26-AUG-1998;	98US-0097951;
PR	26-AUG-1998;	98US-0097952;
PR	26-AUG-1998;	98US-0097955;
PR	26-AUG-1998;	98US-0097955;
PR	26-AUG-1998;	98US-0097971;
PR	26-AUG-1998;	98US-0097974;
PR	26-AUG-1998;	98US-0097978;
PR	26-AUG-1998;	98US-0097979;
PR	26-AUG-1998;	98US-0097986;
PR	26-AUG-1998;	98US-0098014;
PR	31-AUG-1998;	98US-0098525;
PR	16-SEP-1998;	98US-0100634;
PR	12-JAN-1999;	99US-0115565;
XX		
PA	(GETH) GENENTECH INC.	
PI	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK,	
PI	Wood WL, Yuan J;	
XX		
DR	WPI, 2000-072883/06.	
DR	N-PSDB; AAZ65023.	

Query Match	100.0%;	Score 81;	DB 21;	Length 185;
Best Local Similarity	100.0%;	Pred. No. 0.0034;		
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
QY	1 KRLOGKPGCPGPPK 14			
Db	104 KRLOGKPGCPGPPK 117			
RESULT 5				
AAAB65209				
ID	AAAB65209 standard; Protein; 185 AA.			
XX	AAAB65209;			
AC				
XX				
DT	02-APR-2001 (first entry)			
XX				
DE				
XX				
KM	Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.			
KM	Human: secreted and transmembrane protein; PRO; cytosolic;			
KM	cell death; cancer; chromosomal mapping; gene mapping; tissue typing;			
XX	diagnostic assay.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200073454-A1.			
XX				
PD	07-DEC-2000.			
XX				
PF	30-MAR-2000; 2000OMO-US08439.			
XX				
XX				
02-JUN-1999;	99WO-US12252.			
23-JUN-1999;	99US-0141037.			
07-JUL-1999;	99US-0143048.			
26-JUL-1999;	99US-0144758.			
28-JUL-1999;	99US-0145698.			
17-AUG-1999;	99US-0146222.			
15-SEP-1999;	99WO-US21090.			
15-SEP-1999;	99WO-US21547.			
08-OCT-1999;	99US-0158663.			
30-NOV-1999;	99WO-US28313.			
01-DEC-1999;	99WO-US28301.			
16-DEC-1999;	99WO-US30095.			
20-DEC-1999;	99WO-US30911.			
05-JAN-2000;	2000OMO-US00219.			
06-JAN-2000;	2000OMO-US00376.			
11-FEB-2000;	2000OMO-US03565.			
18-FEB-2000;	2000OMO-US04341.			
22-FEB-2000;	2000OMO-US04414.			
24-FEB-2000;	2000OMO-US04914.			

PR	24-FEB-2000;	2000WO-US05004.
PR	02-MAR-2000;	2000WO-US05841.
PR	15-MAR-2000;	2000WO-US06884.
PR	20-MAR-2000;	2000WO-US07377.
XX		
PA	(GETH)	GENENTECH INC.
XX		
PI	Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
PI	Ferrara N, Fong S, Geiber H, Gerritsen ME, Goddard PJ;	
PI	Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;	
PI	Roy MA, Stewart VA, Tumas D, Watanabe CK, Williams PM, Wood W;	
PI	Zhang Z;	
XX		
DR	WPI: 2001-032160/04.	
DR	N-PSDB: AAF44169.	
XX		
PT	PRO polynucleotides used to produce polypeptides used to target	
PT	bioactive molecules such as toxins, radiolabels or antibodies, to	
PT	specific cells, to cause targeted cell death -	
XX		
PS	Claim 12; Fig 139; 935pp; English.	
XX		
CC	The present invention describes human secreted and transmembrane PRO	
CC	proteins. The PRO proteins have cytosolic activity. The PRO proteins	
CC	can be used for targeted delivery of bioactive molecules, such as	
CC	toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide	
CC	sequences, and their fragments, can be used as hybridisation probes, in	
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA	
CC	and DNA. They may also be used to produce transgenic animals which are	
CC	used to develop and screen therapeutically useful reagents. The PRO	
CC	nucleotide and protein sequence can be used for tissue typing and in	
CC	treating cancer. Anti-PRO antibodies can be used in diagnostic assays.	
CC	AA4442720 to AAF44470 represent PCR primers and hybridisation probes used	
CC	in the isolation of human PRO sequences. AAF44087 to AAF44269 and	
CC	AA65154 to AAB65300 represent human PRO polynucleotide and protein	
CC	sequences given in the exemplification of the present invention.	
XX		
S0	Sequence	185 AA:
	Query Match	100.0%; Score 81; DB 22; Length 185;
	Best Local Similarity	100.0%; Pred. No. 0.0034;
	Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 KKLGGKPGCGPPK 14	
DB	104 KKLGGKPGCGPPK 117	
RESULT 6		
AAB50957		
ID	AAB50957 standard; Protein; 185 AA.	
AC	AAB50957;	
XX		
DT	21-MAR-2001 (first entry)	
XX		
DE	Human PRO1005 protein.	
XX		
KW	Human; PRO; cytosolic; neutrotrophic; neuroprotective; respiratory general;	
KW	antitumour; antitumorigenic; immunosuppressive; immunostimulant;	
KW	PRO agonist; cancer; inflammatory disorder; immunological disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200073348-A2.	
XX		
PD	07-DEC-2000.	
XX		
PF	30-MAY-2000; 2000WO-US14941.	
XX		
PR	02-JUN-1999; 99WO-US12252.	
PR	22-JUN-1999; 99US-0140650.	
PR	23-JUN-1999; 99US-0141037.	

PR	20-JUL-1999;	99US-0144758.
PR	01-SEP-1999;	99WO-US20111.
PR	08-SEP-1999;	99WO-US20594.
PR	29-OCT-1999;	99US-0162506.
PR	30-NOV-1999;	99WO-US28313.
PR	01-DEC-1999;	99WO-US28634.
PR	02-DEC-1999;	99WO-US28551.
PR	16-DEC-1999;	99WO-US30095.
PR	20-DEC-1999;	99WO-US30999.
PR	06-JAN-2000;	2000WO-US00376.
PR	11-FEB-2000;	2000WO-US03565.
PR	18-FEB-2000;	2000WO-US04341.
PR	18-FEB-2000;	2000WO-US04342.
PR	02-MAR-2000;	2000WO-US05841.
PR	03-MAR-2000;	2000US-0187202.
PR	10-MAR-2000;	2000WO-US06319.
PR	15-MAR-2000;	2000WO-US06884.
PR	30-MAR-2000;	2000WO-US08439.
PR	17-MAY-2000;	2000WO-US13705.
XX		
PA	(GFTH) GENENTECH INC.	
PI	Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;	
PI	Shelton DL, Smith V, Watanabe CK, Wood WI;	
XX		
DR	WPI: 2001-016509/02.	
DR	N-PSDB; AAC91559.	
XX		
PT	Twenty eight nucleic acids encoding PRO polypeptides which are useful	
PT	for treating various tumors, e.g. breast cancer, and other	
PT	inflammatory, angiogenic and immunological disorders -	
XX		
PS	Claim 31; Fig 14; 188pp; English.	
XX		
CC	The present sequence is one of twenty eight novel PRO polypeptides. The	
CC	PRO polypeptides and their agonists, including antibodies, peptides, and	
CC	small molecule agonists, may be used to treat various tumours, e.g.,	
CC	cancers such as breast cancer, ovarian cancer, renal cancer, colorectal	
CC	cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,	
CC	central nervous system cancer, melanoma or leukaemia. They are also	
CC	useful for treating other disorders such as neuronal, glial, astrocytal,	
CC	hypothalamic and other glandular, macrophagal, epithelial, stromal and	
CC	biostoeolic disorders, and inflammatory, angiogenic and immunological	
CC	disorders.	
XX		
XX		
SQ	Sequence 185 AA;	
	Query Match 100.0%; Score 81; DB 22; Length 185;	
	Best Local Similarity 100.0%; Pred. No. 0.0034;	
	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 KKLGGKGGGPPPK 14	
DB	104 KKLGGKGGGPPPK 117	
RESULT 7		
ABB95492		
ID	ABB95492 standard; Protein: 185 AA.	
XX		
AC	ABB95492;	
XX		
DT	19-JUL-2002 (first entry)	
XX		
DE	Human angiogenesis related protein PRO1005 SEQ ID NO: 140.	
XX		
KW	Human: angiogenesis; PRO protein: cardiovascularisation; wound; cancer;	
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;	
KW	cardiac; cystostatic; antiangiogenic; hypotensive; vulnerary;	
KW	antiarteriosclerotic.	
XX		
OS	Homo sapiens.	
XX		

MO200208284-A2.

31-JAN-2002.

09-JUL-2001; 2001WO-US21735.

20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220624P.

25-JUL-2000; 2000US-220664P.

28-JUL-2000; 2000WO-US20710.

02-AUG-2000; 2000US-222695P.

17-AUG-2000; 2000US-0643657.

23-AUG-2000; 2000WO-US233522.

24-AUG-2000; 2000WO-US233328.

07-SEP-2000; 2000US-230978P.

15-SEP-2000; 2000US-000000P.

18-SEP-2000; 2000US-0664610.

18-SEP-2000; 2000US-0665350.

24-OCT-2000; 2000US-243922P.

08-NOV-2000; 2000US-0709238.

08-NOV-2000; 2000WO-US30952.

10-NOV-2000; 2000WO-US30873.

01-DEC-2000; 2000WO-US32678.

20-DEC-2000; 2000US-0747259.

20-DEC-2000; 2000WO-US34956.

22-JAN-2001; 2001US-0767609.

28-FEB-2001; 2001US-0796498.

28-FEB-2001; 2001WO-US06560.

01-MAR-2001; 2001WO-US06666.

09-MAR-2001; 2001US-0802706.

14-MAR-2001; 2001US-0808689.

22-MAR-2001; 2001US-0816744.

05-APR-2001; 2001US-0828366.

10-MAY-2001; 2001US-0854208.

25-MAY-2001; 2001US-0854280.

25-MAY-2001; 2001US-0866028.

25-MAY-2001; 2001US-0866034.

25-MAY-2001; 2001WO-US17092.

30-MAY-2001; 2001US-0870574.

30-MAY-2001; 2001WO-US17443.

01-JUN-2001; 2001WO-US17800.

20-JUN-2001; 2001WO-US19692.

28-JUN-2001; 2001WO-US00000.

(GETH) GENTECH INC.

(BAKE) BAKER K P.

(FERR) FERRARA N.

(GERB) GERBER H.

(GERR) GERRITSEN M E.

(GODD) GODDARD A.

(GODO) GODDOWSKI P J.

(GURN) GURNEY A L.

(HILL) HILLAN K J.

(MARS) MARSTERS S A.

(PANU) PAN J.

(PAON) PAONI N F.

(STEP) STEPHAN J F.

(WATA) WATANABE C K.

(WILL) WILLIAMS P M.

(WOOD) WOOD W I.

Baker KP, Ferrari N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, N-PSDB: ABL95630.

WPI: 2002-171999/22.

N-PSDB: ABL95630.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

Claim 11: Fig 140: 567pp: English.

PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001US-0870574.
 PR 01-JUN-2001; 2001US-0871780.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2002-090516/12.
 DR N-PSDB: ABL88141.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11: Fig 140; 565pp: English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA:
 Query Match 100.0%; Score 81; DB 23; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRIQKGGPGGPPK 14
 Db 104 KRIQKGGPGGPPK 117
 ID ABL83665 standard; Protein: 185 AA.
 AC ABL83665;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 148.
 XX
 KW Human: secreted protein; PRO: tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 AC
 PD 31-JAN-2002.
 XX

PF 29-JUN-2001; 2001US-0821066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000US-220893P.
 PR 23-AUG-2000; 2000US-223522P.
 PR 24-AUG-2000; 2000US-223522P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000US-0530873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000US-0532678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000US-0534956.
 PR 28-FEB-2001; 2001US-0506520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-08517092.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-172001/22.
 DR N-PSDB: ABR33609.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11: Figure 148; 359pp: English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression in, pericyte cells, for stimulating
 CC the proliferation of, or gene expression in, chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABL83592-ABL83713 represent human PRO
 CC protein sequences of the invention.
 XX
 SQ Sequence 185 AA:
 Query Match 100.0%; Score 81; DB 23; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0034;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRIQKGGPGGPPK 14
 Db 104 KRIQKGGPGGPPK 117
 ID ABL83329 standard; Protein: 186 AA.
 AC ABL83329;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 148.
 XX
 KW Human: secreted protein; PRO: tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 AC
 PD 31-JAN-2002.
 XX

31-JAN-2001 (first entry)

Human secreted protein encoded by gene 9 clone HNSAD53.

Immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; nootropic; antibacterial; virucide; fungicide; opthalmological; human; vulnery; gene therapy; infection; secreted protein.

Homo sapiens.

MO200061623-A1.

19-OCT-2000.

06-APR-2000; 2000WO-US08979.

09-APR-1999; 99US-0128693.

26-APR-1999; 99US-0130991.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppel DR, Shi Y, Lafleur DM, Olsen HS, Ebner R, Florence KA, Moore PA, Blise CE, Young PE.

WPI: 2000-647418/62.

New nucleic acid molecules encoding 62 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 11; Page 598; 716pp; English.

Sequences AAB38321-B38396 represent the amino acid sequences of 62 human secreted proteins encoded by the genes AAC6512-C65187. The genes conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) autoimmune diseases e.g. rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms of the breast or liver; (c) cardiovascular disorders e.g. cardiac arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e) angiodemiasis; (f) nervous system disorders e.g. Alzheimer's disease; (g) infections caused by bacteria, viruses and fungi; and (h) ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis.

Sequence 186 AA;

Query Match 100.0%; Score 81; DB 21; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KRLGKPGCGPPK 14
|||||
104 KRLGKPGCGPPK 117

RESULT 11
ID AAW69974 standard; Protein: 194 AA.
XX AAW69974;
AC AAW69974;
XX 16-NOV-1998 (first entry)
DT Cancer associated protein.
XX

Cancer; PCR; Northern blotting; ribonuclease protection assay;
diagnosis; metastatic cancer.

Synthetic.

WO9837187-A1.

27-AUG-1998.

18-FEB-1998; 98WO-JP00667.

21-FEB-1997; 97JP-0052508.

(TAKI) TAKARA SHUZO CO LTD.

Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;

WPI: 1998-467552/40.

Detection of cancer cells in tissue samples - by changes in mRNA expression compared to normal tissue of specific cancer-associated gene sequences

Claim 14; Page 64-65; 92pp; Japanese.

The cancer associated proteins AAW69974-W69976 where used in the method of the invention to detect cancer cells in tissue samples or biological fluids. They are detected by monitoring the change in mRNA expression as compared to normal tissue of one or more cancer-associated genes whose cDNA stringently hybridises to cancer associated gene nucleic acid fragments. The change in expression may be an increase or a decrease compared to normal tissue. The mRNA expression may be determined by PCR, Northern blotting or ribonuclease protection assay, or by determining the change in the amount of protein encoded by the gene(s) as compared to normal tissue, for example by using a labelled antibody recognising the protein. Detection of cancer cells for cancer diagnosis, including detection of metastatic cancer cells in tissues other than the primary tumour site.

Sequence 194 AA;

Query Match 100.0%; Score 81; DB 19; Length 194;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KRLGKPGCGPPK 14
|||||
113 KRLGKPGCGPPK 126

RESULT 12
ID AAY76591 standard; Protein: 194 AA.
XX AAY76591;
AC AAY76591;
XX 10-APR-2000 (first entry)
DT Human ovarian tumor EST fragment encoded protein 87.
XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;
KW gene therapy; treatment.
XX Homo sapiens.
OS
XX DE19817557-A1.
XX 21-OCT-1999.
PD 09-APR-1998; 98DE-1017557.
PF 09-APR-1998; 98DE-1017557.
XX 09-APR-1998; 98DE-1017557.
PR
XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI: 1999-591920/51.

DR N-PSDB: AA277487.

PT New nucleic acid sequences expressed in ovarian, and some other, cancer

PT tissues, and derived polypeptides, for treatment of ovarian cancer and

PT identification of therapeutic agents -

PS Claim 25; Page 279; 310pp: German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which
XX have anticancer activity and are highly expressed in ovarian tumor
XX tissue (and some also in testis and breast cancer tissue). The products
XX of the invention can be used for gene therapy. (A) are used (i) for
XX recombinant expression of polypeptides (B) and (ii) to isolate complete
XX genes. (B) are used (i) to identify agents suitable for treatment of
XX ovarian cancer; (ii) directly for treating this form of cancer
XX (including expression from gene therapy vectors) and (iii) for generation
XX of specific antibodies. (A) are identified by assembling ESTs (expressed
XX sequence tags) from a particular tissue type before comparison of the
XX expression patterns. This allows a significantly longer fragment of the
XX gene to be revealed, so should reduce the number of failures associated
XX with the fact that ESTs from different libraries may represent different
XX parts of the same unknown gene, distorting the estimated frequency of
XX occurrence in a particular tissue. AA76505-V76638 represent protein
XX fragments encoded by the human ovarian tumor cDNA library derived EST
XX fragments represented in AA277450-277572.

SO Sequence 194 AA;

Query Match 100.0%; Score 81; DB 20; Length 194;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPPK 14

Db 113 KKLGGKGGGPPPK 126

RESULT 13

ID AAB41048 standard; Protein: 103 AA.

AC AAB41048;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.

XX Human: open reading frame; ORFX: detection: cytostatic; hepatotropic;
XX vulnery; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
XX immunostimulant; osteopathic; antiarthritic; immunosuppressant; cardiant;
XX hypotensive; dermatological; coagulant; vasotropic; antidiabetic;
XX antiviral; antibacterial; antifungal; antineoplastic; antiinflammatory;
XX antianaemic; gene therapy; cancer; proliferative disorder; hyperthyroid;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
XX thrombosis; contraceptive.

OS Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shimkels RA, Leach M;

XX WPI: 2000-602362/57.

XX N-PSDB: AAC75257.

PT Novel nucleic acids and peptides derived from open reading frame X,

PT useful for treating e.g. cancers, proliferative disorders,

PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 1306; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;
XX antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
XX antidiabetic; hypotensive; dermatological; immunosuppressive;
XX antineoplastic; antibacterial; antiviral; antifungal; antineuritic;
XX antihypertensive; and antianaemic. The sequences can be used for determining
XX the presence of or predisposition to, or preventing or treating
XX pathological conditions associated with an ORFX-associated disorder. The
XX nucleic acids can be used to express ORFX proteins in gene therapy
XX vectors. The proteins and nucleic acids may be used to treat cancers,
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,
XX graft vs host disease, cardiovascular disease, diabetes mellitus,
XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,
XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
XX nocturnal haemoglobinuria, antiinflammatory disease; to enhance
XX coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 103 AA;

Query Match 64.2%; Score 52; DB 21; Length 103;

Best Local Similarity 64.3%; Pred. No. 12;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPPK 14

Db 61 KKLGGKGGGPPPK 74

RESULT 14

ID AAB35077 standard; Protein: 103 AA.

AC AAB35077;

DT 08-JUL-2002 (first entry)

XX Human ORFX ORF4050 protein, SEQ ID NO:8100.

XX Human: ORFX: open reading frame; ORFX: drug screening; diagnosis;
XX disease monitoring; cytokine; cell proliferation; cell differentiation;
XX immune modulation; haematopoiesis regulation; tissue growth;
XX angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; tumour inhibition; bodily characteristics; fertility;
XX behaviour; cancer; proliferative disorder; neurological disorder;
XX cardiovascular disease; immune system disorder; organ transplantation;
XX tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
XX hypothyroidism; cholesterol ester storage disease; infection; vulnery;
XX vasotropic; antiproliferative; antidiabetic; cytostatic; neurotropic;

KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiac; hypotensive; antihypertensive; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.
 OS Homo sapiens.
 PN WO200190366-A2.
 PD 29-NOV-2001.
 PF 24-MAY-2001; 2001WO-US17076.
 PR 24-MAY-2000; 2000US-206690P.
 PA (CURA-) CURAGEN CORP.
 PI Leach MD, Shimkets RA;
 DR WIPI: 2002-106200/14.
 DR N-PSDB: ABN79103.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation -
 PS Claim 10; Page 2271; 2508pp; English.

CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening individuals for a predisposition to an
 CC activity, and methods of screening individuals for a predisposition to a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, hematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, tumour inhibition activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration, ester
 CC diseases such as diabetes mellitus, hypohydridism, and cholesterol,
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.

XX Sequence 103 AA:

Query Match 64.2%; Score 52; DB 23; Length 103;
 Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPK 14
 DB 61 KKSGGKGGNPRK 74

RESULT 15
 ID AAO01151 standard; Protein: 163 AA.
 AC AAO01151:
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 15043.
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo sapiens.
 PN WO200164835-A2.
 PD 07-SEP-2001.
 PF 26-FEB-2001; 2001WO-US04927.
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 PA (HYSEQ-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 DR WIPI: 2001-514838/56.
 DR N-PSDB: AAI81082.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 PS Claim 20; SEQ ID NO 15043; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, immunomodulatory activity and
 CC activity, tissue growth factor activity, haemostatic activity and/or
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 163 AA:

Query Match 64.2%; Score 52; DB 22; Length 163;
 Best Local Similarity 69.2%; Pred. No. 18;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 KKLGGKGGGPPK 13
 DB 57 KKRGKGGKNNPP 69

Search completed: April 11, 2003, 16:11:08
 Job time : 4.92822 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 11, 2003, 16:07:08 ; Search time 10.8059 Seconds

(Without alignments) 706.250 Million cell updates/sec

Title: US-09-821-726a-16

Perfect score: 993

Sequence: 1 MKLTMFVGLGLAALAPGFA.....TADILWLMSFCGTSVENV 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	993	100.0	184	1	C1IP_MOUSE
2	640	64.5	199	1	C1IP_HUMAN
3	91	9.2	553	1	FXC1_HUMAN
4	89	8.7	345	1	EFBI_MOUSE
5	86	8.6	538	1	PPCK_SALTY
6	85.5	8.6	335	1	CHM1_BOVIN
7	85.5	8.6	346	1	EFBI_HUMAN
8	85.5	8.6	539	1	PPCK_SALTY
9	85	8.6	345	1	EFBI_HUMAN
10	84.5	8.5	334	1	CHM1_MOUSE
11	84	8.5	752	1	HYSA_PROAC
12	83.5	8.4	347	1	CHM1_CHICK
13	81	8.2	553	1	FXC1_MOUSE
14	80.5	8.1	728	1	KDC1_ARATH
15	80	8.1	555	1	P263_RAT
16	79.5	8.0	539	1	PPCK_YERPE
17	79	8.0	336	1	EFBI_MOUSE
18	77.5	7.8	407	1	CHM1_RAT
19	77.5	7.7	407	1	CHM1_MOUSE
20	76.5	7.7	193	1	RPI1_YEAST
21	76.5	7.7	484	1	CSR2_CHICK
22	76	7.7	775	1	GUNA_XANCP
23	75.5	7.6	775	1	ECCL_HUMAN
24	75.5	7.6	193	1	CSR2_MOUSE
25	75	7.6	421	1	YB1U_ECOLI
26	74.5	7.5	334	1	CHM1_HUMAN
27	74.5	7.5	404	1	FTPL_YEAST
28	74	7.5	747	1	YEM1_YEAST
29	74	7.5	775	1	ECCL_MOUSE
30	73	7.4	775	1	ECCL_RAT
31	72.5	7.3	465	1	MTR6_HUMAN
32	72	7.3	409	1	YG4S_YEAST
33	72	7.3	333	1	CHM1_RABIT
			333	1	EFBI_HUMAN

34	72	7.3	367	1	CSP_PLAYO
35	72	7.3	762	1	ECCL_RAT
36	72	7.3	993	1	TSH_DROME
37	71.5	7.2	540	1	PPCK_ECCL
38	71.5	7.2	590	1	MP4_MYXL
39	71.5	7.2	770	1	VP4_ROT9
40	71	7.2	192	1	CSR2_HUMAN
41	71	7.2	544	1	PYRC_ECCL
42	71	7.2	719	1	NRP1_YEAST
43	71	7.2	822	1	EPSS_HUMAN
44	71	7.2	1196	1	AMYB_PABPO
45	71	7.2	1782	1	VIT_BOMMO

ALIGNMENTS

RESULT 1
ID C1IP_MOUSE STANDARD; PRT: 184 AA.
AC Q9GR36; Q9D7K7; Q9CTZ5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C1IP_MOUSE homology.
GN C1IP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RP [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Yashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
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CC
CC EMBL; AK008990; BAB26010.1; -
CC EMBL; AK008622; BAB25784.1; -
CC EMBL; AK008641; BAB25801.1; -
CC EMBL; AK008647; BAB25805.1; -
CC EMBL; AK008722; BAB25856.1; -
CC EMBL; AK008745; BAB25872.1; -
CC EMBL; AK008933; BAB25975.1; -
CC EMBL; AK008956; BAB25988.1; -
CC EMBL; AK009145; BAB26103.1; -
CC EMBL; AK019050; BAB31525.1; -

DR MGD: MGI:1913533; 2200002K21R1K.
 FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 SQ SEQUENCE 184 AA: 20134 MW: 288982F0404FFAB8 CRC64;
 Query Match 100.0%; Score 993; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 4,3e-88;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLTMFVVGILGLLAPGFAYTVNNGNDGVSGGQSVSTNGVHNANVINDNNQMD5 60
 DB 1 MKLTMFVVGILGLLAPGFAYTVNNGNDGVSGGQSVSTNGVHNANVINDNNQMD5 60
 QY 61 NSLMDYENSFAATRLFSKSKSCIVHRMKNKDAMP5LDDLTMTVEQKSGCGAPPKDLMT5 120
 DB 61 NSLMDYENSFAATRLFSKSKSCIVHRMKNKDAMP5LDDLTMTVEQKSGCGAPPKDLMT5 120
 QY 121 VNPTRVEDLNTFGPKIAGMCRGIPYVAEIPGPNOPLYSKKCYTADIIILMRSFGT5 180
 DB 121 VNPTRVEDLNTFGPKIAGMCRGIPYVAEIPGPNOPLYSKKCYTADIIILMRSFGT5 180
 QY 181 VETV 184
 DB 181 VETV 184

RESULT 2
 CLIP_HUMAN STANDARD; PRT; 199 AA.
 ID CLIP_HUMAN
 AC 09NS71:
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CALL protein.
 GN Call.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RX MEDLINE=20296773; PubMed=10835488;
 RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
 RT Isolation of two novel genes, down-regulated in gastric cancer.";
 RL Jpn. J. Cancer Res. 91:459-463(2000).
 CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is
 detected in cancer tissue or gastric cancer cell lines.
 CC -----
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 CC -----
 DR EMBL: AB039886; BAA92433.1; -
 DR MIM: 606402; -
 DR SEQUENCE 199 AA: 21999 MW: C099BBB9A138D7A CRC64;
 SQ

Query Match 64.5%; Score 640; DB 1; Length 199;
 Best Local Similarity 63.8%; Pred. No. 3,1e-54;
 Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMFVVGILGLLAPGFAYTVNNGNDGVSGGQSVSTNGVHNANVINDNNQMD5 59
 DB 1 MKLTMFVVGILGLLAPGFAYTVNNGNDGVSGGQSVSTNGVHNANVINDNNQMD5 59
 QY 15 MKFTTVPACLLVFAALPALANVINVA-DNNNAGSGGQSVSNENNVANVINDNNQMD5 73
 DB 15 MKFTTVPACLLVFAALPALANVINVA-DNNNAGSGGQSVSNENNVANVINDNNQMD5 73
 QY 60 NSLMDYENSFAATRLFSKSKSCIVHRMKNKDAMP5LDDLTMTVEQK--GKGGAPPKDL 117
 DB 60 NSLMDYENSFAATRLFSKSKSCIVHRMKNKDAMP5LDDLTMTVEQK--GKGGAPPKDL 117
 QY 74 WMSIMDYGNFGAFATRLFOKKTCLVHKMKREVMPSIOGLDALYKREKKLOGKGGPPPKGL 133
 DB 74 WMSIMDYGNFGAFATRLFOKKTCLVHKMKREVMPSIOGLDALYKREKKLOGKGGPPPKGL 133
 QY 118 WSVNPTREVDLNTFGPKIAGMCRGIPYVAEIPGPNOPLYSKKCYTADIIILMRSFC 177

DB 134 MYSVNPENKVDLSKFGKNIANMCRGIPYVAEIPGPNOPLYSKKCYTADIIILMRSFC 193
 QY 178 GTSVE 182
 DB 194 GDTVE 198

RESULT 3
 FCX1_HUMAN STANDARD; PRT; 553 AA.
 ID FCX1_HUMAN
 AC 012948; Q9UP06; Q9NUE5; Q9BYM1; Q9UD00;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Forkhead box protein C1 (Forkhead-related protein FKHL7) (Forkhead-
 DE related transcription factor 3) (FREAC-3).
 DE FOXC1 OR FKHL7 OR FREAC3.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS S-112; M-126 AND L-131.
 RX MEDLINE=98282091; PubMed=9620769;
 RA Nishimura D.Y., Swiderski R.E., Alward W.L.M., Searby C.C.,
 RA Patel S.R., Bennet S.R., Kanis A.B., Gastler J.M., Stone E.M.,
 RA Sheffield V.C.;
 RT "The forkhead transcription factor gene FKHL7 is responsible for
 RT glaucoma phenotypes which map to 6p25.";
 RL Nat. Genet. 19:140-147(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS ARA THR-82 AND MET-87.
 RX MEDLINE=99011252; PubMed=9792859;
 RA Mears A.J., Jordan T., Mirzayans F., Dubois S., Kume T., Parlee M.,
 RA Ritch R., Koop B., Kuo W.-L., Collins C., Marshall J., Gould D.B.,
 RA Pearce W., Carlsson P., Enerbaeck S., Moissette J., Bhattacharya S.,
 RA Hogen B., Raymond V., Walter M.A.;
 RT "Mutations of the forkhead/winged-helix gene, FKHL7, in patients with
 RT Axenfeld-Rieger anomaly.";
 RL Am. J. Hum. Genet. 63:1316-1328(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Patel R.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 68-177 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=93271467; PubMed=8499623;
 RA Hromas R., Moore J., Johnston T., Socha C., Klemes M.;
 RT "Prophila forkhead homologues are expressed in a lineage-restricted
 RT manner in human hematopoietic cells.";
 RL Blood 81:2854-2859(1993).
 RN [5]
 RP SEQUENCE OF 73-178 FROM N.A.
 RX MEDLINE=95045392; PubMed=7957066;
 RA Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
 RT "Cloning and characterization of seven human forkhead proteins:
 RT binding site specificity and DNA bending.";
 RL EMBL J. 13:5002-5012(1994).
 CC -1- FUNCTION: BINDING OF FREAC-3 AND FREAC-4 TO THEIR COGNATE SITES
 CC RESULTS IN BENDING OF THE DNA AT AN ANGLE OF 80-90 DEGREES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues and cell lines
 CC examined.
 CC -1- DISEASE: DEFECTS IN FOXC1 ARE THE CAUSE OF A SPECTRUM OF GLAUCOMA
 CC PHENOTYPES SUCH AS AXENFELD-RIEGER ANOMALY (ARA), AXENFELD-RIEGER
 CC SYNDROME (ARS) AND IRIDOGONIOSGENESIS ANOMALY (IGDA). ARS IS AN
 CC AUTOSOMAL DOMINANT DISORDER PRESENTING WITH ARA-LIKE OCULAR
 CC FINDINGS IN ADDITION TO ABNORMALITIES OF THE TEETH, JAW AND
 CC UMBILICUS.
 CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.

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 DR EMBL: AF048693; AAC18081.1; -
 DR EMBL: AF078096; AAC72915.1; -
 DR EMBL: AL034344; CAB81658.1; -
 DR EMBL: L12143; AKI3575.1; -
 DR EMBL: U13221; AAA92038.1; -
 DR HSSP: Q63245; 2HFH.
 DR TRANSFAC: T02471; -
 DR Genew: HGNC:3800; FOXCL.
 DR MIM: 601090; -
 DR MIM: 601631; -
 DR InterPro: IPR001766; TF_Fork_head.
 DR Pfam: PF00250; Fork_head_3.
 DR Prodom: PD000425; TF_Fork_head_1.
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PROSITE: PS50039; FORK_HEAD_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation;
 KW Disease mutation.
 FT DNA_BIND 77 168 FORK-HEAD.
 FT DOMAIN 28 33 POLY-ALA.
 FT DOMAIN 169 173 POLY-ARG.
 FT DOMAIN 194 197 POLY-PRO.
 FT DOMAIN 262 272 POLY-SER.
 FT DOMAIN 292 297 POLY-PRO.
 FT DOMAIN 375 382 POLY-GLY.
 FT DOMAIN 438 445 POLY-SER.
 FT DOMAIN 447 456 POLY-GLY.
 FT DOMAIN 486 495 POLY-ALA.
 FT VARIANT 82 82 S->T (IN ARA).
 FT VARIANT 87 87 /FTID=VAR..007944.
 FT VARIANT 112 112 I->M (IN ARA).
 FT VARIANT 126 126 F->S (IN IGDA).
 FT VARIANT 131 131 /FTID=VAR..007815.
 FT VARIANT 131 131 I->M (IN ARA).
 FT VARIANT 131 131 S->L (IN ARA).
 FT CONFLICT 70 77 OROPKDMV->RSRPRHG (IN REF. 4).
 FT CONFLICT 101 101 L->Q (IN REF. 4).
 FT CONFLICT 180 180 V->L (IN REF. 2).
 FT CONFLICT 199 202 RQPP->ASPR (IN REF. 2).
 FT CONFLICT 426 426 D->N (IN REF. 1).
 SQ SEQUENCE 553 AA; 56788 MW; 59C6FB94303ED59A CRC64;
 Query Match 9.2%; Score 91; DB 1; Length 553;
 Best Local Similarity 19.6%; Pred. NO. 0.43;
 Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;

RESULT 4
 EMBL_MOUSE STANDARD: PRT: 345 AA.
 AC P52795;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ephrin-B1 precursor (Eph-related receptor tyrosine kinase ligand 2)
 DE (LEKX-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
 DE (CEK5-L).
 GN EFNB1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95203867; PubMed=7896266;
 RA Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
 RA Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
 RT "Genomic organization and chromosomal localization of mouse Epl92, a
 RT gene encoding a binding protein for the receptor tyrosine kinase
 RT elk.";
 RL Genomics 24:127-132(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95377533; PubMed=7649373;
 RA Bouillet P., Oulad-Abdelghani M., Violette S., Garnier J.M.,
 RA Schaubaur B., Dolle P., Chambon P.;
 RT "Efficient cloning of cDNAs of retinoic acid-responsive genes in p19
 RT embryonal carcinoma cells and characterization of a novel mouse gene,
 RT Stra1 (mouse LEKX-2/Epl92).";
 RL Dev. Biol. 170:420-433(1995).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95014510; PubMed=7929389;
 RA Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
 RT "cDNA cloning and characterization of a ligand for the CEK5 receptor
 RT protein-tyrosine kinase.";
 RL J. Biol. Chem. 269:26606-26609(1994).
 [4]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1367-1410(2000).
 CC -1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL
 CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
 CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS.
 CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB1 AND EPHA1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR PLATE CELLS.
 CC SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
 CC THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
 CC LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE FLOOR PLATE THROUGHOUT THE
 CC PERIOD OF COMMISSURAL AXON PATHFINDING.
 CC -1- PTM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
 CC CYTOPLASMIC DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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DR EMBL; U07602; AAC53247.1; JOINED.
DR EMBL; U07598; AAC53247.1; JOINED.
DR EMBL; U07599; AAC53247.1; JOINED.
DR EMBL; U07600; AAC53247.1; JOINED.
DR EMBL; U07601; AAC53247.1; JOINED.
DR EMBL; U12983; CA88695.1; -.
DR MGD; MGI:102708; EfnD1.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin.
DR PRINTS; PR01347; Ephrin.
DR PRODOM; PD002533; Ephrin.
DR PROSITE; PS01299; Ephrin.
KW Developmental protein; Neutrogenesis; Transmembrane; Glycoprotein;
FT Signal; Phosphorylation.
FT CHAIN 1 24 POTENTIAL.
FT DOMAIN 25 345 EPHRIN-B1.
FT TRANSMEM 237 257 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 258 345 POTENTIAL.
FT DOMAIN 343 345 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 139 139 PDZ RECOGNITION MOTIF (POTENTIAL).
FT CONFLICT 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 345 AA; 37859 MW; 8C96FD3DC5BCA05 CRC64;

Query Match 9.0%; Score 89; DB 1; Length 345;
Best Local Similarity 23.1%; Pred. No. 0.38; Indels 50; Gaps 10;
Matches 40; Conservative 26; Mismatches 57;

OY 16 ADFGATVTVINGNDGNDGSG---GQSVSINGVHNVANIDNNGWDSNLMYDENSEFA 71
DB 199 AGG-----RSGQSDGDKHERVNDQEKSGPGAGGGGSDSDSEFNSKVAL-----FA 241

OY 72 ARLRSKSKCIV-----HRANKAMPSELQDDITVWKKCKGKPGGAP 113
DB 242 AV---GACGCVFLLLITFTVLLLRKKRRKHTQDRAALSLSTLSPGSGTAGTE 297

OY 114 PKDLMSVNPTRFEDINTFGR---KIAGMCRGIPTYVAEEIPGNP--LYSK 161
DB 298 PDDIILPLRTE---NNYCPHEKYSVG-DYGHVYIVQEMP-POSTANITYK 344

RESULT 5
PCKK_SALTY STANDARD: PRT; 538 AA.
ID PCKK_SALTY STANDARD: PRT; 538 AA.
AC P41033:
DT 01-FEB-1995 (rel. 31, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxylase [ATP] (EC 4.1.1.49) (PEP
DE carboxylase) (Phosphoenolpyruvate carboxylase) (PEPCK).
OS PCKK OR PCK OR STM3500.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
OX 111
RX STRAIN=LT2 / SSGC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RA LT2."
RL Nature 413:852-856(2001).
RP STRAIN=LT2.
RC SEQUENCE OF 251-538 FROM N.A.
RX MEDLINE=89011922; PubMed=2845093;

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RA Listerium P., Laanen I., Palva E.T.;
RT "Structure and expression of the omp operon, the regulatory locus
RT for the outer membrane porin regulon in Salmonella typhimurium
RT Lt-2."
RL J. Mol. Biol. 201:663-673(1988).
RN [3]
RP IDENTIFICATION.
RX MEDLINE=91072271; PubMed=1701430;
RA Medina V., Pontarollo R., Glaeske D., Tabel H., Goldie H.;
RT "Sequence of the pckA gene of Escherichia coli K-12: relevance to
RT genetic and allosteric regulation and homology of E. coli
RT phosphoenolpyruvate carboxylase with the enzymes from Trypanosoma
RT brucei and Saccharomyces cerevisiae."
RL J. Bacteriol. 172:7151-7156(1990).
CC -1- CATALYTIC ACTIVITY: ATP + oxaloacetate = ADP + phosphoenolpyruvate
CC + CO(2).
CC -1- ENZYME REGULATION: ALLOSTERICALLY ACTIVATED BY CALCIUM.
CC -1- POSITIVELY REGULATED BY CAMP (BY SIMILARITY).
CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
CC FAMILY.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
CC in position 363, 458 and 530.
CC
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CC
DR EMBL; AE008861; AAL2362.1; -.
DR EMBL; X12374; -. NOT_ANNOTATED_CDS.
DR HSSP; P22259; 1A02.
DR StyGene; SG10497; pck.
DR InterPro; IPR001272; PEPCK_ATP.
DR Pfam; PF01293; PEPCK_ATP.1.
DR TIGRFAMs; TIGR00224; PCKA.1.
DR PROSITE; PS00532; PEPCK_ATP.1.
KW Gluconeogenesis; Lyase; Decarboxylase; ATP-binding; Calcium;
KW Allosteric enzyme; Complete proteome.
FT NP_BIND 247 254 ATP (BY SIMILARITY).
FT SEQUENCE 538 AA; 59576 MW; 8502FF986D22860A CRC64;

Query Match 8.7%; Score 86; DB 1; Length 538;
Best Local Similarity 23.5%; Pred. No. 1.3; Indels 56; Gaps 11;
Matches 47; Conservative 32; Mismatches 65;

OY 1 MKLTMEFVV--GILGLIAPFAVTVYVINGNDGNV-----DGGQSVSINGVHNVANID 52
DB 210 MKKMFVSNVNYLLPLKGLISMHCSANV-GEKGVAAVFFGLSGTKTTLSTDPRLRLIG-D 267
OY 53 NNNGWSNLSMDYENS-FAATRLFEKSKS--CLVHRANKDAMS----- 93
DB 268 DEHGWD--DGVNFEFGGCAKTIKLSKEAPEIYHAIRPALLANVTYREDGTVDFPDGS 326
OY 94 -----LQDDITVWKKCKGKGP-----GGAPPKDLMSVNPTRFEDINTF 132
DB 327 KIENRVSVPITYIHIDITVAVSKAGHATVIFLTADFGVLPVSRKLTANOTQYHFLSGF 365
OY 133 GPKIAGMCRGI---PTYVA 148
DB 386 TAKLAGTERGVTEPPTPSA 405

RESULT 6
CHM1_BOVIN STANDARD: PRT; 335 AA.
ID CHM1_BOVIN STANDARD: PRT; 335 AA.
AC P17404; P23590;
DT 01-AUG-1990 (rel. 15, Created)

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GN EFNBI OR EPLG2 OR LERK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95022634; PubMed=7936648;
 RA Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
 RA Gimpel S., Hollingsworth T., Vandenbos T., Davison B.L.,
 RA Lyman S.D., Beckmann M.P.,
 RT "LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
 RT evolutionarily conserved and expressed in a developmentally regulated
 RT pattern.";
 RL Oncogene 9:3241-3248(1994).
 CC -1- FUNCTION: BINDS TO, AND INDUCE THE COLLAPSE OF, COMMISSURAL
 CC AXONS/GROWTH CONES IN VITRO. MAY PLAY A ROLE IN CONSTRAINING THE
 CC ORIENTATION OF LONGITUDINALLY PROJECTING AXONS (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHB3 (PREFERRED),
 CC EPHB1 AND EPHB2.
 CC -1- PPM: INDUCIBLE PHOSPHORYLATION OF TYROSINE RESIDUES IN THE
 CC CYTOPLASMIC DOMAIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
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 CC EMBL: U07560; AAA55092.1;
 CC Interpro: IPR001799; Ephrin.
 DR Pfam: PF00812; Ephrin.1.
 DR PRINTS: PRO1347; EPHRIN.
 DR PRODOM: PD002533; Ephrin.1.
 DR PROSITE: PS01299; EPHRIN.1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24
 FT CHAIN 25 345
 FT DOMAIN 25 236
 FT TRANSMEM 237 257
 FT DOMAIN 258 345
 FT DOMAIN 343 345
 FT CARBOHYD 139 139
 SO SEQUENCE 345 AA: 37951 MW: 183045557358F7E CRC64;
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-1045557358F7E CRC64;
 Query Match 8.6%; Score 85; DB 1; Length 345;
 Best Local Similarity 23.1%; Pred. No. 0.91;
 Matches 40; Conservative 24; Mismatches 59; Indels 50; Gaps 10;
 QY 16 AGFAATVYINNDQNVOS-----GQOVSINGVHNVANIDNNGDSNNSLMDYENSFA 71
 DB 195 APG-----KSGQSDSCKEHTVNOEKSFGAGSGSGDIDSPNSVAL-----FA 241
 QY 72 ATFLFSKSCVY-----HRMKNKDMPSLDDLOTWYKQKGGKGGAP 113
 DB 242 AV-----GAGCVIFLLIFLVLLKLRKRKRKQQAALSLSTLSPKDSCTAGTE 297
 QY 114 PKDLMSYNPRTVELNFTFGP---KIACMGKGIPTVVAEEIIPGPQP---LYSK 161
 DB 298 PSDIITPLKTE-----NNYCPHYEKVSG-DYGHVYIVQEMP-PQSPANIYK 344
 RESULT 10
 CHM1_MOUSE
 ID CHM1_MOUSE STANDARD; PRT; 334 AA.
 AC 0921F6; 090XU5; PRT; 334 AA.
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chondromodulin-I precursor (Chm-I) (Leukocyte cell-derived chemotaxin
 DE 1) [Contains: Chondrosurfactant protein (Ch-SP)].
 GN CHM1 OR LECT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hiraki Y., Shukunami C., Inoue H., Suzuki F.,
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RC SRRAIN-C57H/6J; TISSUE=Embryonic head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuoka Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Bifunctional growth regulator that stimulates the growth
 CC of cultured chondrocytes in the presence of basic fibroblast
 CC growth factor (FGF) but inhibits the growth of cultured vascular
 CC endothelial cells. May contribute to the rapid growth of cartilage
 CC and vascular invasion prior to the replacement of cartilage by
 CC bone during endochondral bone development (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
 CC inter-territorial matrix of cartilage (By similarity).
 CC -1- PPM: After cleavage, the post-translationally modified Chm-I is
 CC secreted as a glycoprotein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
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 CC EMBL: U43509; A000027.1;
 DR EMBL: AK013975; BAB29095.1;
 DR MGD: MGI:1341171; Lect1.
 KW Cartilage; Glycoprotein; Transmembrane;
 KW Cleavage on pair of basic residues.
 FT CHAIN 1 210
 FT PROPEP 211 214
 FT CHAIN 215 334
 FT TRANSMEM 46 66
 FT CARBOHYD 243 243
 FT CONFLICT 108 109
 FT CONFLICT 163 163
 FT CONFLICT 207 207
 SO SEQUENCE 334 AA: 37252 MW: DAFDEC43C7D745D6 CRC64;
 CHONDROSURFACTANT PROTEIN
 (BY SIMILARITY).
 CHONDROMODULIN-I (BY SIMILARITY).
 POTENTIAL.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 AK -> FE (IN REF. 2).
 V -> A (IN REF. 2).
 K -> KANFA (IN REF. 2).
 DAFDEC43C7D745D6 CRC64;

Query Match 8.5%; Score 84.5; DB 1; Length 334;
 Best Local Similarity 20.8%; Pred. No. 0.98;
 Matches 31; Conservative 29; Mismatches 64; Indels 25; Gaps 5;

OY 21 YVYVING--NDGNVDSGGQSVSINGVHVNANIDNNNGMDSWNSLMDENSEFAATRFESK 78
 ID 78 YSMKINGKLDGG-----SMEDAVNNLETFKMGSAKEAIEVNFKNIGITGRFAGG 129
 DB 79 KSCIVHRMNDAMPSTLDDLTVMYKQKGGFGAP-----KDLMSVNPTRVEDLNTFG 133
 OY 130 EKYTYAQAQVARIPE---EYGVTVTKQSISELEKGLMPVNYEENSLTWAVDQPKDSFELS 186
 DB 134 PKIAGMCRGIPPTVYAEIPGPNOLYSKK 162
 OY 187 SKIETLGDLPFIFWL-----KPMYPRKE 208

RESULT 11
 ID HSYA_PROAC STANDARD; PRT: 752 AA.
 AC 059634;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hyaluronate lyase precursor (EC 4.2.2.1) (Hyaluronidase) (Hyase).
 OS Propionibacterium acnes.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Propionibacteriaceae; Propionibacteriaceae;
 OC Propionibacterium.
 NC NCB1_TaxID=1747;
 RN [1]
 RP MEDLINE=97270208; PubMed=9115089;
 RA Steiner B.M., Romero-Steiner S., Cruce D., George R.;
 RT "Cloning and sequencing of the hyaluronate lyase gene from
 RT Propionibacterium acnes.";
 RL Can. J. Microbiol. 43:315-321(1997).
 CC -1- CATALYTIC ACTIVITY: Hyaluronate - N 3-(4-deoxy-beta-D-gluc-4-
 CC enuronosyl)-N-acetyl-D-glucosamine.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: CELL-ASSOCIATED.
 CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
 CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
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 CC -----
 CC EMBL: U15927; AAA51650.1; -
 CC Interpro: IPR003159; Lyase_8.
 CC Interpro: IPR004103; Lyase_8.C.
 CC Pfam: PF02278; Lyase_8.C; 1.
 CC Pfam: PF02884; Lyase_8.C; 1.
 CC Lyase: Signal. 1
 CC SIGNAL 32
 CC CHAIN 33 752 HYALURONATE LYASE.
 CC FT CHAIN 33 752 60D5DCA691CA1A4 CRC64;
 CC S0 SEQUENCE 752 AA; 81910 MW; 60D5DCA691CA1A4 CRC64;

Query Match 8.5%; Score 84; DB 1; Length 752;
 Best Local Similarity 24.1%; Pred. No. 3;
 Matches 33; Conservative 18; Mismatches 62; Indels 24; Gaps 6;

OY 15 AARGATVYVINGNCGVSGGQSVSINGVHVNANIDNNNGMDSWNSLMDYENSFAATR 74
 ID 15 AARGATVYVINGNCGVSGGQSVSINGVHVNANIDNNNGMDSWNSLMDYENSFAATR 74
 DB 119 AARGATVYVINGNCGVSGGQSVSINGVHVNANIDNNNGMDSWNSLMDYENSFAATR 166
 OY 75 LFSKSCIVHRMNDAMP-----SLDDLTVMYKQKGGFGAPPPDLIMSVNPTRVED 128
 DB 167 AVADVNCILH-----DVLPRPVMSAAAGIDHFIIPDPWFQOPGVSKP--TANPVPVSTG 220

OY 129 INTFGPKIAGMCRGIPPT 145
 DB 221 ANRMDLTRAVMCRSIAT 237

RESULT 12
 ID CHM1_CHICK STANDARD; PRT: 347 AA.
 AC 09PUB8; Q9Y163;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chondromodulin-I precursor (Chm-I) [Contains: Chondrosurfactant
 DE protein (Ch-Sp)].
 GN CHM1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9031;
 RN [1]
 RP MEDLINE=20058447; PubMed=10590475;
 RA Dietz U.H., Zieglmeier G., Blüthner K., Bruckner P., Bailing R.;
 RT "Spatio-temporal distribution of Chondromodulin-I mRNA in the chicken
 RT embryo: Expression during cartilage development and formation of the
 RT heart and eye.";
 RL Dev. Dyn. 216:233-243(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Retal sternum;
 RX MEDLINE=99379620; PubMed=10452551;
 RA Shukunami C., Yamamoto S., Tanabe T., Hiraki Y.;
 RT "Generation of multiple transcripts from the chicken chondromodulin-I
 RT gene and their expression during embryonic development.";
 RL FEBS Lett. 456:165-170(1999).
 CC -1- FUNCTION: Bifunctional growth regulator. May contribute to the
 CC rapid growth of cartilage and vascular invasion prior to the
 CC replacement of cartilage by bone during endochondral bone
 CC development (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
 CC interterritorial matrix of cartilage (by similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in the cartilage and in fetal
 CC prearticular tissues as well as in heart and eye.
 CC -1- DEVELOPMENTAL STAGE: Expression onset occurs between stage 10 and
 CC stage 13.
 CC -1- PTM: After cleavage, the post-translationally modified Chm-I is
 CC secreted as a glycoprotein (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
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 CC -----
 CC EMBL: AF138280; AAD32212.1; -
 CC EMBL: AF027380; AAD08642.1; -
 CC Cartilage: Glycoprotein; Transmembrane;
 CC Cleavage on pair of basic residues.
 CC CHAIN 1 209 CHONDROSURFACANT PROTEIN
 CC FT CHAIN 1 209 (BY SIMILARITY).
 CC FT PROPEP 210 213 POTENTIAL.
 CC FT CHAIN 214 347 CHONDROMODULIN-I.
 CC FT TRANSSEM 45 65 POTENTIAL.
 CC FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 250 250 D -> E (IN REF. 2).
 CC S0 SEQUENCE 347 AA; 38636 MW; F3C5FE3385D4B66 CRC64;

Query Match 8.4%; Score 83.5; DB 1; Length 347;
 Best Local Similarity 19.6%; Pred. No. 1.3;

Matches 37; Conservative 27; Mismatches 68; Indels 57; Gaps 7;

OY 4 TMEVGLGLGLAAP-----GFATVING--NGDNVDSGQSVSINGVH 46
 Db 44 TVLIAGALLLACAGATGATKATEROVNVHVTMSINGKVOD-----SMEIDAGN 95
 OY 47 NVANIDNNCWDSMNSIMDYENSFAATRLFSKSCIVHRNKAMPGLDLDITVKEOKG 106
 Db 96 NLETFKTSGSSEBAVEHDFDQIGTGRFAGKEKCYTKAPKARP---EVDAMTK--- 148
 OY 107 KGGGAPPPDLMSVNPTRVEDLNT-----FGPRAGMCRGIPYVAEIP 152
 Db 149 -----ASLSSDLEDEIMPVREDNSLIWVADEPIKHNGLFSPKILFELGDLPIFWL----- 200
 OY 153 GPNQPLYSK 161
 Db 201 ---RPYYPK 206

RESULT 13
 EXCL_MOUSE

ID FXCL_MOUSE STANDARD: PRT: 553 AA.
 AC 061572; 061582; 088409;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Forkhead box protein C1 (Forkhead-related protein FKHL7) (Forkhead-related transcription factor 3) (FREC-3) (Transcription factor FKHL-1)
 DE (Mesoderm/mesenchyme forkhead 1) (Mf-1).
 GN FOXC1 OR FKHL7 OR FREAC3 OR FKHL1 OR MFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98297351; PubMed=9635428;
 RA Kume T., Deng K.Y., Wanfey V., Gould D.B., Walter M.A., Hogan B.L.M.;
 RT "The forkhead/winged helix gene Mfl is disrupted in the pleiotropic mouse mutation congenital hydrocephalus.";
 RL Cell 93:985-996(1998).
 RN [2]
 RP SEQUENCE OF 69-179 FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=93361500; PubMed=7689224;
 RA Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H., Monaghan A.P., Schuetz G.;
 RT "Six members of the mouse forkhead gene family are developmentally regulated";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).
 RN [3]
 RP SEQUENCE OF 71-187 FROM N.A.
 RX MEDLINE=93387221; PubMed=8375339;
 RA Sasaki H., Hogan B.L.;
 RT "Differential expression of multiple fork head related genes during gastrulation and axial pattern formation in the mouse embryo.";
 RL Development 118:47-59(1993).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY EMBRYONIC TISSUES, INCLUDING PRECHONDROGENIC MESENCHYME, PERICULAR MESENCHYME, MENINGES, ENDOTHELIAL CELLS, AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.
 CC -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.

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 CC EMBL: AF045017; AAC24209.1; -

DR EMBL: L10406; AAA03159.1; -;
 DR EMBL: X71939; CAA50741.1; -;
 DR HSSP: 063245; ZHH.
 DR TRANSFAC: T02426; -;
 DR MGI: MGI:1347466; Foxc1.
 DR InterPro: IPR001766; TF_Fork_head.
 DR Pfam: PF00250; Fork_head_1.
 DR PRINTS: PR00053; FORKHEAD.
 DR ProDom: PD000425; TF_Fork_head_1.
 DR SMART: SM00339; FH_1.
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PROSITE: PS50039; FORK_HEAD_3; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 FT DOMAIN 28 33
 FT DNA_BIND 77 168
 FT DOMAIN 169 173
 FT DOMAIN 194 197
 FT DOMAIN 264 274
 FT DOMAIN 375 386
 FT DOMAIN 444 451
 FT DOMAIN 453 456
 FT DOMAIN 486 496
 FT CONFLICT 180 186
 SO SEQUENCE 553 AA; 56953 MW; 3CDD12F6CA4F217 CRC64;
 VKDKERK -> KKEITFI (IN REF. 3).

Query Match
 Best Local Similarity 19.8%; Score 81; DB 1; Length 553;
 Matches 38; Conservative 21; Mismatches 61; Indels 72; Gaps 9;

OY 14 LAAPGFATVINGNDGNDVDSGQSVSINGVHNA-----NIDNNNGW----- 57
 Db 76 MKPPYSTIALIT---MAIONAPDKKITLNGIYOFIMDFPPYRDNKQGWQMSIRHNLSL 132
 OY 58 -----DSNNSIMDYENS--FAATRLFSKSCIVHRNKDAM 91
 Db 133 NECFKVPBRDCKPKPGSGVWTLDPSTNM---FENGSEFLRRRRRKKDAVDKKEKGR 189
 OY 92 PSLDLDITMVEQKGGGCGAPPPKDLMSV-----NPTREVDLNFPGPKIGMCGIGT 146
 Db 190 -----HLOPPPPQAGROPAPAPPEQAGSAPQOPPPYRIDIKTEN-----GTC----- 235
 OY 147 VAEIIPGNPL 158
 Db 236 -----PSPPOPL 242

RESULT 14
 KDGL_ARATH STANDARD: PRT: 728 AA.

ID KDGL_ARATH
 AC 039017; 09SD92;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Diacylglycerol kinase 1 (EC 2.7.1.107) (Diacylceride kinase 1)
 DE (DGK 1) (DAG kinase 1).
 GN DGK1 OR ATSG07920 OR P13G24.120 OR MXM12.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=96189276; PubMed=8605313;
 RA Katagiri T., Mizoguchi T., Shinzaki K.;
 RT "Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in Arabidopsis thaliana.";
 RL Plant Mol. Biol. 30:647-653(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

RA MEDLINE-21016721; PubMed-1130714; Kotani H., Kato T., Asamizu E.,
 RA Tabata S., Kaneko T., Nakamura Y., Hosouchi T., Kawashima K.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno S., Muraki A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shino S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Habermann K., Murray J., Johnson D., Kohlring T., Nelson J.,
 RA Stoeckert T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney J., Dante M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
 RA Wagner-McPherson C., Mollam A., Yeakum M., Bell M., Dedina N.,
 RA Parnell L., Shan R., Rodriguez M., Hoon See L., Vill D., Baker J.,
 RA Kirchhoff K., Toth K., King L., Banret A., Miller B., Marra M.,
 RA Martensen R., McCombie W.R., Wilsson R.K., Murphy G., Bancroft I.,
 RA Volckert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Ertlan K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymopreuz B., Zimmermann W.,
 RA Ramsparger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirke W., Koolman P., Klein Lankhorst R.,
 RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berner S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel S., Gielen J., Ardies W.,
 RA Berts O., Lemcke K., Kolesov G., Mayer K.F.X., Rued S., Schoof H.,
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RT thaliana." ;
 RT Nature 408:823-826(2000).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN-CV. Columbia;
 RC MEDLINE-97471969; PubMed-9330910;
 RX Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT DNA Res. 4:215-230(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol - ADP + 1,2-
 CC diacylglycerol 3-phosphate.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS, AND LEAVES.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
 CC FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHOSBO-ESTER AND DAG
 CC BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL: D63787; BAA09856.1; -
 CC EMBL: AL133421; CAB62604.1; -
 CC EMBL: AB005249; BAB09956.1; -
 CC InterPro: IPR000756; DAGKa.
 CC InterPro: IPR001206; DAGKc.
 CC InterPro: IPR002219; DAG-pe-bind.
 CC InterPro: IPR003622; DAG_kin_cat.
 CC Pfam: PF00609; DAGKa.1.
 CC Pfam: PF00781; DAGKc.1.
 CC ProDom: PD002939; DAGKa.1.
 CC ProDom: PD005043; DAG_kin_cat.1.
 CC SMART: SM00109; C1; 2.
 CC SMART: SM00045; DAGKa.1.
 CC SMART: SM00046; DAGKc.1.
 CC PROSITE: PS00479; DAG-pe BIND DOM.1; FALSE_NG.
 CC PROSITE: PS00481; DAG-pe BIND DOM.2; 2.
 CC TRANSFAM: Kinase; Phospho-ester binding; Transmembrane; Repeat.
 CC TRANSMEM 27 48 POTENTIAL.

FT DOMAIN 95 137 PHOSBO-ESTER AND DAG BINDING 1.
 FT DOMAIN 169 212 PHOSBO-ESTER AND DAG BINDING 2.
 FT DOMAIN 359 490 CATALYTIC (POTENTIAL).
 FT DOMAIN 507 664 CATALYTIC (POTENTIAL).
 FT CONFLICT 509 509 N -> T (IN REF. 1).
 FT SEQUENCE 728 AA; 79983 MW; 9E3190721C0830E9 CRC64;
 Query Match 8.1%; Score 80.5; DB 1; Length 728;
 Best Local Similarity 24.1%; Pred. No. 6.2;
 Matches 34; Conservative 27; Mismatches 7;
 QY 27 GNGC-NVDSGQSOVS-SINGVH-----NVANIDNNNGDSNMSLMDYNSFAATR 74
 DB 275 GNGSNDTESTHADTCPIVNGAHAVLENSISVYNGSDSSGDSNCKLEKRSYKRTG 334
 QY 75 LPSKSCIVHRMKNDAPILODLDT-----WYEGKRGKPGGAPPKDLMYSNPTRVE 127
 DB 335 SFGQKE--YHALRSKILYELADLPDSARPPLVFLINKSGAQRGSRLHLHNPQVVF 392
 QY 128 DLNTE-GPKIA-GMCRGIPTV 146
 DB 393 ELSSVQGPVGLFLFRKVPHF 413
 RESULT 15
 ID F263_RAT STANDARD; PRT; 555 AA.
 AC 035552; 035553; 035554; 035555; 035556; 035557; 090W05; 090W06;
 AC 035096;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (6PF-2-K/Fru-
 DE 2,6-P2KSE brain-type isozyme) (RB2K) [includes: 6-phosphofructo-2-
 DE kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)].
 GN PRKFB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP STRAIN-Sprague-Dawley; TISSUE=Brain;
 RC MEDLINE-97345796; PubMed-9202288;
 RX Watanabe F., Sakai A., Furuya E.;
 RA "Novel isoforms of rat brain fructose 6-phosphate 2-kinase/fructose
 RT 2,6-bisphosphatase are generated by tissue-specific alternative
 RT splicing." ;
 RT J. Neurochem. 69:1-9(1997).
 RL [2]
 RN SEQUENCE OF 61-369 FROM N.A.
 RP STRAIN-Wistar; TISSUE=Placenta;
 RC Sakakibara R.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SYNTHESIS AND DEGRADATION OF FRUCTOSE 2,6-BISPHOSPHATE.
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate - ADP + D-
 CC fructose 2,6-bisphosphate.
 CC -1- CATALYTIC ACTIVITY: D-fructose 2,6-bisphosphate + H(2)O - D-
 CC fructose 6-phosphate + phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1/RB2K1 (SHOWN HERE), 2/RB2K2,
 CC 3/RB2K3, 4/RB2K4, 5/RB2K5, 6/RB2K6, 7/RB2K7 AND 8/RB2K8; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
 CC PHOSHOGLYCERATE MUTASE FAMILY.
 CC -----
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DR EMBL; D87240; BAA21749.1; -
 DR EMBL; D87241; BAA21750.1; -
 DR EMBL; D87242; BAA21751.1; -
 DR EMBL; D87243; BAA21752.1; -
 DR EMBL; D87244; BAA21753.1; -
 DR EMBL; D87245; BAA21754.1; -
 DR EMBL; D87246; BAA21755.1; -
 DR EMBL; D87247; BAA21756.1; -
 DR EMBL; AB006710; BAA22048.1; -
 DR InterPro: IPR000546; 6PF2K.
 DR InterPro: IPR003094; 6PF2K.
 DR InterPro: IPR001345; PG/BPGM_mutase.
 DR pfam; PF00300; PGAM; 1.
 DR pfam; PF01591; 6PF2K; 1.
 DR PRINTS; PR00991; 6PF2K; 1.
 DR PRODOM; PD002665; 6PF2K; 1.
 DR PROSITE; PS00175; PG_MUTASE; 1.
 KW Multifunctional enzyme; Transferase; Kinase; Hydrolase; ATP-binding;
 KW Phosphorylation; Multigene family; Alternative splicing.
 FT DOMAIN 1 245
 FT NP_BIND 246 555
 FT BINDING 42 49
 FT BINDING 99 99
 FT ACT_SITE 190 190
 FT ACT_SITE 125 125
 FT ACT_SITE 155 155
 FT ACT_SITE 254 254
 FT ACT_SITE 323 323
 FT ACT_SITE 388 388
 FT VARSPIC 448 476
 FT VARSPIC 543 555
 FT VARSPIC 535 555
 FT VARSPIC 543 555
 FT CONFLICT 185 185
 FT CONFLICT 367 367
 SQ SEQUENCE 555 AA; 63675 MW; 45B2D090B44FCDBD CRC64;

Query Match Best Local Similarity 24.88; Score 80; DB 1; Length 555;

Matches 26; Conservative 17; Mismatches 42; Indels 20; Gaps 4;

OY 79 KSCIVHRMNDAM-----PSLODLDTM---VKEGKGKPGGAPPKDL---MYS 120
 Db 437 ESYSTRERESEAVKIQHFASVVRSSVTELDPLVESAKODAKKGNPLMRNSVTPPLAS 496
 OY 121 VNFTREVDLNTFGPKTAGMGRCIPTYVAEEIPG--PNQPLYSKKC 163
 Db 497 PEPTKPKRINSFEHVASTSAALPSCLPPEVPRQLPGQPLGKAC 541

Search completed: April 11, 2003, 16:11:59
 Job time : 12.9725 secs

